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Database :
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8:  em_htc:*
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14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
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19: em_gss_pln:*
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24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

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28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
	1	715.2	63.1	1740	11	BC035686		BC035686	Homo sapi
c	2	701.4	61.9	886	13	BX433093		BX433093	BX433093
c	3	659.2	58.2	899	13	BX433092		BX433092	BX433092
	4	561.4	49.5	753	29	AY420885		AY420885	Homo sapi
	5	530.4	46.8	3470	11	AK048781		AK048781	Mus muscu
	6	530.4	46.8	3729	11	AK038551		AK038551	Mus muscu
	7	519.8	45.9	1790	11	BC035858		BC035858	Homo sapi
	8	519.4	45.8	3153	11	AK079572		AK079572	Mus muscu
c	9	504.4	44.5	790	14	CF147830		CF147830	AGENCOURT
	10	474.2	41.9	750	29	AY420886		AY420886	Pan trogl
	11	472	41.7	1001	9	AL535838		AL535838	AL535838
	12	468.6	41.4	726	29	AY420887		AY420887	Mus muscu
	13	393.2	34.7	993	12	BM926746		BM926746	AGENCOURT
	14	374.6	33.1	543	13	BX119589		BX119589	BX119589
	15	367	32.4	788	14	CF147829		CF147829	AGENCOURT
	16	329.2	29.1	382	12	BQ042116		BQ042116	sheep1 Sh
c	17	296	26.1	525	12	BI133700		BI133700	UI-M-BH3-
	18	285.4	25.2	635	12	BM939496		BM939496	UI-M-BH3-
	19	278.4	24.6	520	13	BQ269289		BQ269289	ik23f12.y
	20	265.8	23.5	627	10	BB632359		BB632359	BB632359
	21	265.4	23.4	599	12	BM933820		BM933820	UI-M-BH3-
	22	263.2	23.2	611	13	BY723922		BY723922	BY723922
	23	249	22.0	892	13	BX409735		BX409735	BX409735
	24	216.8	19.1	477	12	BM087401		BM087401	500158 MA
	25	202.4	17.9	662	10	BB632883		BB632883	BB632883
c	26	198.4	17.5	625	13	BQ285933		BQ285933	ik23f12.x
	27	198.2	17.5	1073	12	BM920548		BM920548	AGENCOURT
	28	197.6	17.4	505	10	BB651179		BB651179	BB651179
	29	196.8	17.4	245	12	BI976482		BI976482	485407 MA
	30	186.2	16.4	464	13	BY239887		BY239887	BY239887
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c	32	165.8	14.6	703	29	CE375359		CE375359	tigr-gss-
	33	163.2	14.4	1290	29	AY411591		AY411591	Homo sapi
	34	162	14.3	721	29	CE235359		CE235359	tigr-gss-
	35	157.8	13.9	1296	29	AY411593		AY411593	Mus muscu
c	36	156.2	13.8	1013	9	AL535837		AL535837	AL535837
	37	147.2	13.0	768	13	BX109847		BX109847	BX109847
	38	133	11.7	257	10	AW427900		AW427900	64510 MAR
c	39	127.2	11.2	1005	28	CC212654		CC212654	CH261-75F
c	40	127.2	11.2	1058	28	CC297061		CC297061	CH261-177
c	41	122.4	10.8	1194	28	CC279941		CC279941	CH261-24C
	42	120.2	10.6	526	29	CG978334		CG978334	CH240 169
	43	119	10.5	1113	29	AY420480		AY420480	Homo sapi
	44	117.8	10.4	1100	29	AY420481		AY420481	Pan trogl
	45	108.8	9.6	1113	29	AY420482		AY420482	Mus muscu

## ALIGNMENTS

## RESULT 1

BC035686

LOCUS BC035686 1740 bp mRNA linear HTC 20-SEP-2002

DEFINITION Homo sapiens, Similar to hypocretin (orexin) receptor 1, clone  
IMAGE:5750551, mRNA.

ACCESSION BC035686

VERSION BC035686.1 GI:23242909

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1740)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USAREMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 79 Row: m Column: 17

This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 4557636

This clone has the following problem: frame shifted.

## FEATURES

source

Location/Qualifiers

1. .1740

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5750551"

/tissue\_type="Lung, Spleen, fetal, pooled"

/clone\_lib="NIH\_MGC\_122"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 63.1%; Score 715.2; DB 11; Length 1740;  
Best Local Similarity 83.3%; Pred. No. 4.8e-139;  
Matches 906; Conservative 0; Mismatches 3; Indels 179; Gaps 1;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      506 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 565

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db      566 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 625

Qy     121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
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Db     626 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 685

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db     686 CTGGTGGGCAACACGCTG----- 703

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
Db     704 ----- 703

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
Db     704 ----- 703

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db     704 -----GGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 746

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db     867 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 926

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
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 Db 1107 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 1166  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
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 Db 1167 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1226  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
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 Db 1227 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1286  
 Qy 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 1287 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1346  
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 Db 1347 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1406  
 Qy 1081 CTCAGTGG 1088  
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 Db 1407 CTCAGTGG 1414

## RESULT 2

BX433093/c

LOCUS BX433093 886 bp mRNA linear EST 15-MAY-2003

DEFINITION BX433093 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
 CS0DF013YE04 3-PRIME, mRNA sequence.

ACCESSION BX433093

VERSION BX433093.1 GI:30779168

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 886)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 151.r For  
 more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0BAI011ZB01\\_CS00962\\_2&cluster=151.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_2&cluster=151.r).

Contact : Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01\_CS00962\_2.

FEATURES  
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 Location/Qualifiers  
 1. .886  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /tissue\_type="FETAL BRAIN"  
 /dev\_stage="fetal"  
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 /note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 61.9%; Score 701.4; DB 13; Length 886;  
 Best Local Similarity 99.0%; Pred. No. 2.8e-136;  
 Matches 705; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy	377	AGGCTGTGTCCGTGTCTAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT	436
Db	745	AGGCTGTGTCCGTGTCTAGTGACAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT	686
Qy	437	ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGCGGGCCCGTGGCTCCATCC	496
Db	685	ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGCGGGCCCGTGGCTCCATNC	626
Qy	497	TGGGCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA	556
Db	625	TGGGCATCTGGCCTGTGTCTGCTGGCCATCATGGTGCCCAGGGCTGCAGTCATGCAATGCA	566
Qy	557	GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT	616
Db	565	GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT	506
Qy	617	GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGG	676
Db	505	GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGG	446
Qy	677	CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC	736
Db	445	CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC	386
Qy	737	AGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGCCCCCTCAGACCAGCTGG	796
Db	385	AGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGCCCCCTCAGACCAGCTGG	326
Qy	797	GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTG	856
Db	325	GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTG	266
Qy	857	AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTCTGG	916
Db	265	AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTCTGG	206
Qy	917	TCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGGTGTTTCGGGA	976

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Db      205 TCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGA. 146

Qy      977 TGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGC 1036
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Qy      1037 TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTCCTCAGTGG 1088
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Db      85 TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTCCTCAGTGG 34

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RESULT 3

BX433092/c

LOCUS BX433092 899 bp mRNA linear EST 15-MAY-2003

DEFINITION BX433092 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
CS0DF013YE04 3-PRIME, mRNA sequence.

ACCESSION BX433092

VERSION BX433092.1 GI:30779167

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 899)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 151.r For  
more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0BAI011ZB01\\_CS00962\\_1&cluster=151.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_1&cluster=151.r).

Contact : Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01\_CS00962\_1.

FEATURES

Location/Qualifiers

source

1. .899

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DF013YE04"

/tissue\_type="FETAL BRAIN"

/dev\_stage="fetal"

/clone\_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

ORIGIN

Query Match

58.2%; Score 659.2; DB 13; Length 899;

Best Local Similarity 94.4%; Pred. No. 1.9e-127;  
Matches 693; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

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Qy      372 TCTACAGGCTGTGTCCGTGTTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCG 431
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Db      738 TGTAAGNNCTGTGTCTGTTCAGTGGCAGTGCTACTTCTCAGCTTCATCGCCTGGACCCG 679

Qy      432 CTGGTATGCCATC-TGCCACCCACTATTGTTCAAGAGCACAGCCCGGGGGCCCGTGGCT 490
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Db      678 CTGGTATGCCATCATCCACCCACTATTGTCAAAGAGCACAGCCCGGGGGCCCGTGGCTC 619

Qy      491 CCATCCTGGGCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGG 550
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Qy      551 AATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATG 610
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Qy      611 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCT 670
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Db      498 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCT 439

Qy      671 ACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCAAGCTCTGGG 730
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Qy      731 GCGGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGCCCCCTCAGACC 790
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Db      378 GCGGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGCCCCCTCAGACC 319

Qy      791 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCC 850
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Qy      851 TGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 910
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Db      258 TGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 199

Qy      911 TGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 970
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Db      198 TGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 139

Qy      971 TCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 1030
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Db      138 TCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 79

Qy      1031 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTCCTCAGTGGAT 1090
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Db      78 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTCCTCAGTGGAA 19

Qy      1091 GTAAAGAGAAGAGT 1104
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Db      18 ATTCCGGGAGCAGT 5

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RESULT 4

AY420885  
 LOCUS AY420885 753 bp DNA linear GSS 17-DEC-2003  
 DEFINITION Homo sapiens HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION AY420885  
 VERSION AY420885.1 GI:39776842  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 753)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 753)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence as made by sequencing genomic exons and ordering them  
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# RESULT 5

AK048781

LOCUS AK048781 3470 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230065B06 product:OREXIN RECEPTOR TYPE 2, full insert sequence.

ACCESSION AK048781

VERSION AK048781.1 GI:26339571

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3470)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genomic Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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ORIGIN

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- Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
- REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636
- REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159
- REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861
- REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)
- REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)
- REFERENCE 6 (bases 1 to 3729)  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,



Db 239 GGGTCCTGATCGCAGGGTATATCATCGTGTTCGTTGTGGCTCTCATCGGGAACGTCCTGG 298  
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 Qy 860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGGTGGTGGTCT 919  
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 Db 920 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 979  
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 Db 980 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1039  
 Qy 980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039  
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 Db 1040 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1099  
 Qy 1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTCCTCAGTGG 1088  
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 Db 1100 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGG 1148

# RESULT 8

AK079572

LOCUS AK079572 3153 bp mRNA linear HTC 19-SEP-2003

DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230091E19 product:OREXIN RECEPTOR TYPE 2, full insert sequence.

ACCESSION AK079572

VERSION AK079572.1 GI:26348079

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE

3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3153)  
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
 Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
 Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,  
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 Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,  
 Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,  
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
 Muramatsu,M. and Hayashizaki,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.go.jp/  
 URL:http://fantom.gsc.riken.go.jp/.  
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 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
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 /db\_xref="MGI:2403517"  
 /db\_xref="taxon:10090"  
 /clone="A230091E19"  
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YPKMYHICFFLVTYMAPLFLMILAYLQIFRKLWCRQIPGTSSVVQRKWKQQQPVSQPR
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# ORIGIN

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Query Match          45.8%; Score 519.4; DB 11; Length 3153;
Best Local Similarity 71.0%; Pred. No. 6.3e-98;
Matches 718; Conservative 0; Mismatches 286; Indels 7; Gaps 2;

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Db      211 ACGACGAGGAATTCCCTGCGGTACCTGTGGAGGAATACCTACACCCGAAAGAATATGAGT 270

Qy      140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
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Db      271 GGGTCCTGATCGCAGGATATATCATCGTGTTCGTTGTGGCTCTCATCGGGAACGTCCTGG 330

Qy      200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      331 TCTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACAGTCACCAACTACTTCATAGTCA 390

Qy      260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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Db      391 ACCTTTCCCTAGCAGATGTGCTTGTGACCATCACCTGCCTTCCAGCTACCCTCGTTGTTG 450

Qy      320 ACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
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Db      451 ACATCACTGAGACTTGGTTCCTTGGACAGTCCCTCTGTAAGGTCATTTCCTTATTTACAGA 510

Qy      380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
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Db      511 CTGTGTCAAGTGTCTGTGTCTGTTCTTACGTTGAGCTGCATTGCCTTGGACCGATGGTACG 570

Qy      440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Db      571 CCATTTGTCAACCCTTTGATGTTCAAGAGCACAGCCAAACGGGCTCGAAACAGCATCGTTG 630

Qy      500 GCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
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Db      631 TCATCTGGATCGTCTCCTGCATCATAATGATTCCTCAAGCCATTGTCATGGAGTGCAGCA 690

Qy      560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
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Db      691 GCATGCTCCCTGGCCTAGCCAATAAGACCACCCTCTTTACAGTATGTGATGAACACTGGG 750

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Qy	620	CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCCC	679
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Qy	680	CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA	739
Db	811	CTCTGTTTCTTATGATATTGGCTTATCTCCAAATATTCCGTAAACTCTGGTGCCGACAGA	870
Qy	740	TCCCCGGCACCCACCTCAGCACTGGTGCGGAAGCTGGAAGCGCCCCTCAGACCAGCTGGGGG	799
Db	871	TTCCCGAAGTCTTCTGTGGTTCAGAGAAAATGGAAGCAGC-----AGCAGCCGGTTT	924
Qy	800	ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG	859
Db	925	CTCAGCCCCGGGGTCCGGACAGCAGAGCAAGGCTCGGGTTAGCGCTGTTGCTGCTGAGA	984
Qy	860	TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTCTGCTGGTCT	919
Db	985	TAAAGCAGATCCGAGCACGAAGGAAAACAGCCCGGATGCTCATGGTTGTACTTCTGGTCT	1044
Qy	920	TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT	979
Db	1045	TTGCAATTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT	1104
Qy	980	TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG	1039
Db	1105	TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTTCACTTTTCCTCATTGGCTTG	1164
Qy	1040	TGTACGCCAACAGC-GCTGCCAACCCCATCATCTACAACCTTCCTCAGTGG A	1089
Db	1165	TATATGCCAACAGCTGCTGCAAACCCAATTATTTATAATTTTCTTAGTGG A	1215

cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: IRBI02 row: a column: 08

High quality sequence start: 7

High quality sequence stop: 738.

FEATURES  
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/mol\_type="mRNA"  
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/tissue\_type="mixed"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_145"  
/note="Vector: pCDNA3.1; Site\_1: varies by clone; Site\_2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',  
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBI.preSV.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat)  
a Note: this is a NIH\_MGC Library."

#### ORIGIN

Query Match 44.5%; Score 504.4; DB 14; Length 790;  
Best Local Similarity 99.8%; Pred. No. 4.7e-95;  
Matches 505; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      583 CGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATC 642
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Qy      643 TACCACAGTTGCTTCTTTATTGTGACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 702
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Db      730 TACCACAGTTGCTTCTTTATTGTGACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 671

Qy      703 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 762
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Db      670 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 611

Qy      763 GTGCGGAAGTGAAGCGCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 822
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Db      610 GTGCGGAAGTGAAGCGCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 551

Qy      823 GAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGG 882
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Db      550 GAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGG 491

Qy      883 AAGACAGCCAAGATGCTGATGGTGGTGTGCTGCTGCTTCGCCCTCTGCTACCTGCCCATC 942
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Db      490 AAGACAGCCAAGATGCTGATGGTGGTGTGCTGCTGCTTCGCCCTCTGCTACCTGCCCATC 431

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Db      430 AGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 371
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Db      370 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 311
Qy      1063 CCCATCATCTACAACCTTCCTCAGTGG 1088
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Db      310 CCCATCATCTACAACCTTCCTCAGTGG 285

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# RESULT 10

AY420886

LOCUS AY420886 750 bp DNA linear GSS 17-DEC-2003

DEFINITION Pan troglodytes HCRT1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY420886

VERSION AY420886.1 GI:39776843

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 750)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 750)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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## ORIGIN

Query Match 41.9%; Score 474.2; DB 29; Length 750;  
 Best Local Similarity 84.5%; Pred. No. 9.7e-89;  
 Matches 476; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 526 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585  
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Qy 586 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645  
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 Db 61 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 120

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 Db 121 CACAGTTGCTTCTTTATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 180

Qy 706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765  
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 Db 181 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 240

Qy 766 CGGAAGTGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825  
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 Db 241 CGGAAGTGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 300

Qy 826 CCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885  
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 Db 301 CCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 360

Qy 886 ACAGCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 945  
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 Db 361 ACAGCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGT 420

Qy 946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005  
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 Db 421 GTCCTCAATGTCCTTAAGAGNN 480

Qy 1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065  
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 Db 481 NNN 540

Qy 1066 ATCATCTACAACCTTCCTCAGTGG 1088  
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 Db 541 ATCANNNACAACCTTCCTCAGTGG 563

# RESULT 11

AL535838

LOCUS AL535838 1001 bp mRNA linear EST 12-MAY-2003

DEFINITION AL535838 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
 CS0DF013YE04 5-PRIME, mRNA sequence.

ACCESSION AL535838

VERSION AL535838.2 GI:30542758

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1001)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 13, 2001 this sequence version replaced gi:12799331.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 151.r For  
 more information about this cluster, see  
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r)  
[cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r). Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DF013BC02QP1.

FEATURES Location/Qualifiers  
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 /dev\_stage="fetal"  
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 /note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with Not I and  
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 vector. Library was not normalized."

#### ORIGIN

Query Match 41.7%; Score 472; DB 9; Length 1001;  
 Best Local Similarity 92.0%; Pred. No. 3.2e-88;  
 Matches 544; Conservative 13; Mismatches 25; Indels 9; Gaps 6;

Qy	377	AGGCTGTGTCCGTGTCTAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT	436
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Qy	437	ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC	496
Db	475	ATGCHATCTGCTACCCACTATTGTTCAAGARCACAGCCCGGCGGGCCCGTGGCTCCATCC	534
Qy	497	TGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA	556
Db	535	TNNGNATCTGGGCTNTNTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA	594
Qy	557	GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT	616
Db	595	GCAGTGTGCTGCCTNAGCTANCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT	654
Qy	617	GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGG	676
Db	655	GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGG	714
Qy	677	CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCAAGCTCTGGGGCCGCC	736
Db	715	CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCAAGCTCTGGGGCCGCC	774

Qy 737 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAGCGCCCCCTCAGACCAGCT-G 795  
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 Db 775 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAGCGCCCCCTCAGACCAGCTGG 834  
 Qy 796 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCT 855  
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 Db 835 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCC--AGCCCCGGGGCCGCGCCTTCCTGGCT 892  
 Qy 856 GAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTG 915  
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 Db 893 GAAGTGA---RCAGATGSTGCAGGCAGVAGACASCSAAGATGCTGATGGTGGBGCTGCTG 949  
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 Db 950 STCTTCG-CCTCTGCTACSTG-CCATCAGSGT-CTCAATGTCTTAAAGAGG 997

# RESULT 12

AY420887

LOCUS AY420887 726 bp DNA linear GSS 17-DEC-2003

DEFINITION Mus musculus HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY420887

VERSION AY420887.1 GI:39776844

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 726)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 726)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .726  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 gene <1. .>726  
 /gene="HCRTR1"  
 /locus\_tag="HCM7373"

ORIGIN

Query Match 41.4%; Score 468.6; DB 29; Length 726;  
 Best Local Similarity 89.5%; Pred. No. 1.4e-87;  
 Matches 504; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

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Qy      526 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
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Db      1 ATGGTGCCCCAGGCTGCTGTTCATGGAGTGCAGCAGCGTGTGCTGCCTGAGCTAGCCAATCGC 60

Qy      586 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
        || |||||
Db      61 ACCCGGCTCTTCTCAGTCTGTGATGAGCACTGGGCAGATGAACTCTACCCCAAGATCTAT 120

Qy      646 CACAGTTGCTTCTTTATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
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Db      121 CACAGCTGCTTTTTTCATTGTACCTACCTGGCCCCACTGGGCCTCATGGCTATGGCCTAT 180

Qy      706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
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Db      181 TTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCTGGTACCACATCAGCCTTGGTG 240

Qy      766 CGGAAGTGGAAAGCGCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
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Db      241 CGGAAGTGGAAAGCGCCCTCGGAACAACTGGAGGCTCAGCACCAGGGCCTCTGTACAGAG 300

Qy      826 CCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
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Db      301 CCCCAGCCCCGGGGCCGAGCCTTCCTGGCTGAGGTGAAGCAGATGCGAGCTCGGAGGAAG 360

Qy      886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 945
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Db      361 ACGGCTAAGATGCTGATGGTAGTCCTGCTGGTTTTTGCAGTCTGTTATCTGCCCATCAGT 420

Qy      946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
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Qy      1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
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Qy      1066 ATCATCTACAACCTCCTCAGTGG 1088
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Db      541 ATCATCTACAACCTCCTCAGTGG 563
  
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RESULT 13  
 BM926746  
 LOCUS BM926746 993 bp mRNA linear EST 12-MAR-2002  
 DEFINITION AGENCOURT\_6681991 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5767576  
 5', mRNA sequence.  
 ACCESSION BM926746  
 VERSION BM926746.1 GI:19377125  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



Qy	80	ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT	139
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Qy	140	GGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCCCTGGTGGGCAACACGCTGG	199
Db	205	GGGTCTGATCGCCGGTACATCATCGTGTTCGTCTGTCGTGGCTCTCATTTGGGAACGTCCTGG	264
Qy	200	TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA	259
Db	265	TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA	324
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCCTGCCGGCCAGCCTGCTGGTGG	319
Db	325	ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCAGCCACACTGGTCGTGG	384
Qy	320	ACATCACTGAGTCTTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCCTATCTACAGG	379

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Db      385 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCCTTATCTACAGA 444
Qy      380 CTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
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Db      445 CCGTGTCCGTGTCTGTGTCTGTCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 504
Qy      440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGCGGGCCCGTGGCTCCATCCTGG 499
      | |||| | |||| | ||| ||||| ||||| ||||| | || |
Db      505 CAATCTGTCAACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 564
Qy      500 GCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
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Db      565 TCATCTGGATTGTCTCCTGCATTATAATGATTCCCTCAGGCCATCGTCATGGAGTGCAGCA 624
Qy      560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
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Db      625 CCGTGTTCCAGGCTTAGCCAATAAAACCACCTCTTTACGGTGTGTGATGAGCGCTGGG 684
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Db      685 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTCTTTCTGGTGACATACATGGCAC 744
Qy      680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
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Qy      740 TCCCCGGCACCCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCCTCAGAC 789
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#### RESULT 14

BX119589

LOCUS BX119589 543 bp mRNA linear EST 10-FEB-2003

DEFINITION BX119589 Soares infant brain lNIB Homo sapiens cDNA clone  
IMAGp998P20171 ; IMAGE:40608, mRNA sequence.

ACCESSION BX119589

VERSION BX119589.1 GI:28289997

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 543)

AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
Radelof,U., Schneider,D. and Korn,B.

TITLE Human UnigeneSet - RZPD3

JOURNAL Unpublished (2003)

COMMENT Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp998P20171.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human UnigeneSet - RZPD3 (RZPDLIB No.972)

[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972)

[bin/showLib.pl.cgi/response?libNo=972](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972) Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT.

FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGp998P20171 ; IMAGE:40608"  
 /sex="female"  
 /dev\_stage="73 days post natal"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares infant brain 1NIB"  
 /note="Organ: whole brain; Vector: Lafmid BA; Site\_1: Not  
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 I - oligo(dT) primer [5'  
 AACTGGAAGAATTCGCGGCCGACAGGAATTTTTTTTTTTTTTTTTT 3'];  
 double-stranded cDNA was ligated to Hind III adaptors  
 (Pharmacia), digested with Not I and directionally cloned  
 into the Not I and Hind III sites of the Lafmid BA vector.  
 Library went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo."

# ORIGIN

Query Match 33.1%; Score 374.6; DB 13; Length 543;  
 Best Local Similarity 98.7%; Pred. No. 6e-68;  
 Matches 377; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60  
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 Db 158 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 217  
 Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
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 Db 218 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 277  
 Qy 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180  
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 Db 278 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 337  
 Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
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 Db 338 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 397  
 Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
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 Db 398 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 457  
 Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
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 Db 458 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGNAAG 517

Qy 361 GTCATCCCCTATCTACAGGCTG 382  
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 Db 518 GTCATCCCCTATCTACAGACAG 539

RESULT 15  
 CF147829

LOCUS CF147829 788 bp mRNA linear EST 25-JUL-2003

DEFINITION AGENCOURT\_14740210 NIH\_MGC\_145 Homo sapiens cDNA clone  
 IMAGE:6971890 5', mRNA sequence.

ACCESSION CF147829

VERSION CF147829.1 GI:33244097

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 788)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: IRBI02 row: a column: 09

High quality sequence start: 9

High quality sequence stop: 772.

FEATURES

source

Location/Qualifiers

1. .788

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6971890"

/tissue\_type="mixed"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_145"

/note=Vector: pCDNA3.1; Site\_1: varies by clone; Site\_2:  
 varies by clone; ORFs were PCR-amplified and cloned into  
 pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
 clone and include the following: 5'-EcoRV-XmnI/XhoI-3',  
 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).  
 For information about which gene each clones represents,  
 please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBI.preSV.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat)  
 a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match

32.4%; Score 367; DB 14; Length 788;

Best Local Similarity 72.7%; Pred. No. 2.8e-66;  
Matches 472; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

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Qy	140	GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCCCTGGTGGGCAACACGCTGG	199
Db	200	GGGTCCTGATCGCCGGGTACATCATCGTGTTCTGTCGTGGCTCTCATTGGGAACGTCCTGG	259
Qy	200	TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA	259
Db	260	TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA	319
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG	319
Db	320	ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCTGG	379
Qy	320	ACATCACTGAGTCCTGGCTGTTCTGGCCATGCCCTCTGCAAAGTCATCCCCTATCTACAGG	379
Db	380	ATATCACCGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA	439
Qy	380	CTGTGTCCGTGTCTAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG	439
Db	440	CCGTGTCCGTGTCTGTGTCTGTCTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG	499
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGGGGCCGTGGCTCCATCCTGG	499
Db	500	CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCCGTAACAGCATTGTCA	559
Qy	500	GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db	560	TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA	619
Qy	560	GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG	619
Db	620	CTGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTACGGTGTGTGATGAGCGCTGGG	679
Qy	620	CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC	679
Db	680	GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC	739
Qy	680	CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTG	728
Db	740	CACTGTGTCTCATGGTGTGGCTTATCTGNCAATAATTCGCANACTCTG	788

Search completed: October 15, 2004, 22:50:33  
Job time : 3299.03 secs

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:54:41 ; Search time 4590.56 Seconds  
(without alignments)  
10697.520 Million cell updates/sec

Title: US-10-070-532-5  
Perfect score: 1133  
Sequence: 1 atggagccctcagccacccc.....tctgaccatcggtgccccgg 1133

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
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27: em\_sts:\*

28: em\_un:\*  
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 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%					Description
	No.	Score	Match Length	DB	ID	
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3	1131.4	99.9	1133	6	BD185454	BD185454 Human neu
4	1128.2	99.6	1170	6	E43972	E43972 Novel G pro
5	1128.2	99.6	1170	6	AX746118	AX746118 Sequence
6	1114.4	98.4	1116	6	AR216119	AR216119 Sequence
7	1086.4	95.9	1209	6	AR216117	AR216117 Sequence
8	1086.4	95.9	1564	6	E43974	E43974 Novel G pro
9	1086.4	95.9	1564	6	E50810	E50810 Novel G pro
10	1086.4	95.9	1564	6	E50811	E50811 Novel G pro
11	1086.4	95.9	1564	6	AX299473	AX299473 Sequence
12	1086.4	95.9	1564	6	AX299475	AX299475 Sequence
13	1086.4	95.9	1564	6	AX549082	AX549082 Sequence
14	1086.4	95.9	1564	6	AX746121	AX746121 Sequence
15	1086.4	95.9	1564	6	AX840912	AX840912 Sequence
16	1086.4	95.9	1564	9	AF041243	AF041243 Homo sapi
17	1084.8	95.7	1110	6	AR216118	AR216118 Sequence
18	1081.6	95.5	1209	6	BD185452	BD185452 Human neu
19	1081.6	95.5	1278	6	AX280925	AX280925 Sequence
20	1076.8	95.0	1110	6	BD185453	BD185453 Human neu
21	892.8	78.8	2200	10	AY336083	AY336083 Mus muscu
22	891.2	78.7	2469	10	AF041244	AF041244 Rattus no
23	697.6	61.6	843	6	AR109899	AR109899 Sequence
24	670.6	59.2	789	6	AR109632	AR109632 Sequence
25	670.6	59.2	789	6	E12154	E12154 cDNA encodi
26	670.6	59.2	789	6	AR300942	AR300942 Sequence
27	579.6	51.2	781	10	AF394596	AF394596 Mus muscu
28	554.4	48.9	3114	10	AF041246	AF041246 Rattus no
29	530.4	46.8	1545	10	AY336084	AY336084 Mus muscu
30	530.4	46.8	2117	10	AY336085	AY336085 Mus muscu
31	520.8	46.0	1633	6	E33974	E33974 cDNA clone
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33	520.8	46.0	1843	6	AX840914	AX840914 Sequence

34	520.8	46.0	1878	9	AF041245	AF041245 Homo sapi
35	516	45.5	1335	6	AX280927	AX280927 Sequence
36	514.4	45.4	1805	4	AF164626	AF164626 Canis fam
37	496.2	43.8	597	10	AY255599	AY255599 Mus muscu
38	329.2	29.1	382	4	AF499612	AF499612 Ovis arie
39	304.2	26.8	637	10	AF394597	AF394597 Mus muscu
40	281.6	24.9	328	4	AB092488	AB092488 Bos tauru
41	263.2	23.2	501	4	AF532967	AF532967 Ovis arie
42	249.2	22.0	344	9	F202078S03	AF202080 Homo sapi
43	249.2	22.0	9785	6	AR178605	AR178605 Sequence
44	249.2	22.0	9785	6	AX088174	AX088174 Sequence
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# ALIGNMENTS

## RESULT 1

E43973

LOCUS E43973 1133 bp DNA linear PAT 31-JAN-2002

DEFINITION Novel G protein-coupled receptor (HFGAN72Y).

ACCESSION E43973

VERSION E43973.1 GI:18625172

KEYWORDS JP 2000106888-A/2.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1133)

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE Novel G protein-coupled receptor (HFGAN72Y)

JOURNAL Patent: JP 2000106888-A 2 18-APR-2000;

SMITHKLINE BEECHAM CORP

## COMMENT

OS Unidentified

PN JP 2000106888-A/2

PD 18-APR-2000

PF 21-JUL-1999 JP 1999206116

PR 30-APR-1997 US 08/846705

PI DERK J BERGSMA,CATHARINE ELIZABETH ELLIS

PC C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC A61P1/14,

PC A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC A61P13/08,

PC A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,

PC A61P31/04,

PC A61P31/10,A61P31/12,A61P31/18,A61P33/00,A61P35/00,A61P37/08,

PC A61P43/00,

PC C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,

PC G01N33/577//

PC C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,

PC A61K37/02,

PC A61K37/02,C12N5/00,(C12N15/00,C12R1:91)

CC Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1. .1133

FT /organism='Unidentified'.

## FEATURES

Location/Qualifiers



source 1. .1133  
/organism="unidentified"  
/mol\_type="genomic DNA"  
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ORIGIN

Query Match 99.9%; Score 1131.4; DB 6; Length 1133;  
Best Local Similarity 99.9%; Pred. No. 2.2e-218;  
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
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 Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCTGACCATCGTGCCCCGG 1133  
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# RESULT 2

AX746120

LOCUS AX746120 1133 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 3 from Patent EP1156110.

ACCESSION AX746120

VERSION AX746120.1 GI:31744926

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE G-protein coupled receptor (HFGAN72Y)

JOURNAL Patent: EP 1156110-A 3 21-NOV-2001;

SMITHKLINE BEECHAM CORPORATION (US)

FEATURES

source

Location/Qualifiers

1. .1133

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/note="HGS EST 557082"

ORIGIN

Query Match 99.9%; Score 1131.4; DB 6; Length 1133;

Best Local Similarity 99.9%; Pred. No. 2.2e-218;

Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
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Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
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Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
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Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840

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Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
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Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
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Db	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG	1133

RESULT 3

BD185454

LOCUS BD185454 1133 bp DNA linear PAT 17-JUN-2003

DEFINITION Human neuropeptide receptor.

ACCESSION BD185454

VERSION BD185454.1 GI:31877654

KEYWORDS JP 2002360288-A/3.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1133)

AUTHORS Soppet,D.R., Li,Y. and Rosen,C.A.

TITLE Human neuropeptide receptor

JOURNAL Patent: JP 2002360288-A 3 17-DEC-2002;

HUMAN GENOME SCIENCES INC

COMMENT OS Unidentified

PN JP 2002360288-A/3

PD 17-DEC-2002

PF 02-MAY-2002 JP 2002130838

PI DANIEL R SOPPET,YI LI,CRAIG A ROSEN

PC C12N15/09,A61K31/7088,A61K38/00,A61K45/00,A61K48/00,A61P3/04,

PC A61P3/06,

PC A61P3/10,A61P9/10,A61P9/12,A61P25/08,A61P25/18,A61P25/22, PC

A61P25/28,

PC A61P35/00,A61P43/00,C07K14/705,C07K16/24,C12N1/15,C12N1/19, PC

C12N1/21,

PC C12N5/10,C12Q1/68,C12N15/00,C12N5/00,A61K37/02 CC

Strandedness: Single;

CC Topology: Linear;

CC Human neuropeptide receptor

FH Key Location/Qualifiers

FT source 1. .1133

FT /organism='Unidentified'.

FEATURES Location/Qualifiers

source 1. .1133

/organism="unidentified"

/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 99.9%; Score 1131.4; DB 6; Length 1133;  
Best Local Similarity 99.9%; Pred. No. 2.2e-218;  
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGACCCC 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
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Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
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Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db    661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

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Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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#### RESULT 4

E43972

LOCUS E43972 1170 bp DNA linear PAT 31-JAN-2002

DEFINITION Novel G protein-coupled receptor (HFGAN72Y).

ACCESSION E43972

VERSION E43972.1 GI:18625171

KEYWORDS JP 2000106888-A/1.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1170)

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE Novel G protein-coupled receptor (HFGAN72Y)

JOURNAL Patent: JP 2000106888-A 1 18-APR-2000;

SMITHKLINE BEECHAM CORP

COMMENT OS Unidentified

PN JP 2000106888-A/1

PD 18-APR-2000

PF 21-JUL-1999 JP 1999206116

PR 30-APR-1997 US 08/846705

PI DERK J BERGSMA,CATHARINE ELIZABETH ELLIS

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PC A61P31/10,A61P31/12,A61P31/18,A61P33/00,A61P35/00,A61P37/08,

PC A61P43/00,

PC C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,  
PC G01N33/577//  
PC C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,  
PC A61K37/02,  
PC A61K37/02,C12N5/00,(C12N15/00,C12R1:91)  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1. .1170  
FT /organism='Unidentified'.

FEATURES Location/Qualifiers  
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# ORIGIN

Query Match 99.6%; Score 1128.2; DB 6; Length 1170;  
Best Local Similarity 99.7%; Pred. No. 9.6e-218;  
Matches 1130; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
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Db	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
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Db	361	GTCATCCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
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Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540

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Qy	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
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Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
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Db	961	AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Qy	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCTGACCATCGTGCCCCGG	1133
Db	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGCTCTGTCTGCCCATCGTGCCCCGG	1133

# RESULT 5

AX746118

LOCUS AX746118 1170 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 1 from Patent EP1156110.

ACCESSION AX746118

VERSION AX746118.1 GI:31744924

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE G-protein coupled receptor (HFGAN72Y)

JOURNAL Patent: EP 1156110-A 1 21-NOV-2001;  
SMITHKLINE BEECHAM CORPORATION (US)



FEATURES	Location/Qualifiers
source	1. .1170 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
gene	1. .1170 /gene="HFGAN72Y"
CDS	1. .1170 /gene="HFGAN72Y" /codon_start=1 /protein_id="CAD97474.1" /db_xref="GI:31744925" /translation="MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQ YEWVLIAAYVAVFVVALVGNLTVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPA SLLVDITESWLFGHALCKVIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARR ARGSILGIWAVSLAIMVPQAAMECCSVLPELANRTRLFSVCDERWADDLYPKIYHSC FFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEP QPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFQGMFRQASDRE AVYACFTFSHWLVYANSAANPIIYNFLSGCKEKSLLALSCPSCP GHDPHLAAALCS"

# ORIGIN

Query Match 99.6%; Score 1128.2; DB 6; Length 1170;  
 Best Local Similarity 99.7%; Pred. No. 9.6e-218;  
 Matches 1130; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	121	TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480

Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540  
 Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGC 780  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Db 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080

Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCTGACCATCGTGCCCCGG 1133  
 Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCTGACCATCGTGCCCCGG 1133

# RESULT 6

AR216119

LOCUS AR216119 1116 bp DNA linear PAT 25-SEP-2002

DEFINITION Sequence 5 from patent US 6410701.

ACCESSION AR216119

VERSION AR216119.1 GI:23314432

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1116)

AUTHORS Soppet,D.R., Li,Y. and Rosen,C.A.

TITLE Human neuropeptide receptor  
JOURNAL Patent: US 6410701-A 5 25-JUN-2002;  
FEATURES Location/Qualifiers  
source 1. .1116  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 98.4%; Score 1114.4; DB 6; Length 1116;  
Best Local Similarity 99.9%; Pred. No. 5.9e-215;  
Matches 1115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
        |||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGACCCC 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        |||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        |||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        |||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        |||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        |||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        |||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        |||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
        |||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        |||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
        |||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCAGATATTCCGC 720
Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGC 780
Db      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGC 780
Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
Qy      961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
Db      961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
Qy      1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116
Db      1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116

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# RESULT 7

AR216117

LOCUS AR216117 1209 bp DNA linear PAT 25-SEP-2002

DEFINITION Sequence 1 from patent US 6410701.

ACCESSION AR216117

VERSION AR216117.1 GI:23314430

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1209)

AUTHORS Soppet,D.R., Li,Y. and Rosen,C.A.

TITLE Human neuropeptide receptor

JOURNAL Patent: US 6410701-A 1 25-JUN-2002;

FEATURES Location/Qualifiers

source 1. .1209

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1209;

Best Local Similarity 99.9%; Pred. No. 2.7e-209;

Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60

Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900

Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
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 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Qy 1081 CTCAGTGG 1088  
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 Db 1081 CTCAGTGG 1088

RESULT 8

E43974

LOCUS E43974 1564 bp DNA linear PAT 31-JAN-2002

DEFINITION Novel G protein-coupled receptor (HFGAN72Y).

ACCESSION E43974

VERSION E43974.1 GI:18625173

KEYWORDS JP 2000106888-A/3.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1564)

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE Novel G protein-coupled receptor (HFGAN72Y)

JOURNAL Patent: JP 2000106888-A 3 18-APR-2000;

SMITHKLINE BEECHAM CORP

COMMENT OS Unidentified

PN JP 2000106888-A/3

PD 18-APR-2000

PF 21-JUL-1999 JP 1999206116

PR 30-APR-1997 US 08/846705

PI DERK J BERGSMA,CATHARINE ELIZABETH ELLIS

PC C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC

A61P1/14,

PC A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC

A61P13/08,

PC A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,

PC A61P31/04,

PC A61P31/10,A61P31/12,A61P31/18,A61P33/00,A61P35/00,A61P37/08,

PC A61P43/00,

PC C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,

PC G01N33/577//

PC C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,

PC A61K37/02,

PC A61K37/02,C12N5/00,(C12N15/00,C12R1:91)

CC Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1. .1564

FT /organism='Unidentified'.  
 FEATURES Location/Qualifiers  
 source 1. .1564  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;  
 Best Local Similarity 99.9%; Pred. No. 2.6e-209;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	274	TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCG	720

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAGCGC 780
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAGCGC 933

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233

Qy      1081 CTCAGTGG 1088
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Db      1234 CTCAGTGG 1241

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# RESULT 9

E50810

LOCUS E50810 1564 bp DNA linear PAT 18-JUN-2001

DEFINITION Novel G protein-bound receptor (HFGAN 72X).

ACCESSION E50810

VERSION E50810.1 GI:13023197

KEYWORDS JP 2000060578-A/1.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1564)

AUTHORS Derk, J.B. and Catharine, E.E.

TITLE Novel G protein-bound receptor (HFGAN 72X)

JOURNAL Patent: JP 2000060578-A 1 29-FEB-2000;

SMITHKLINE BEECHAM CORP

COMMENT OS Unidentified

PN JP 2000060578-A/1

PD 29-FEB-2000

PF 21-JUL-1999 JP 1999206115

PR 30-APR-1997 US 08/846704

PI DERK J BERGSMA, CATHARINE ELIZABETH ELLIS

PC C12N15/09, A61K31/70, A61K38/00, A61K39/00, A61K39/395, A61K39/395,

PC A61K45/00,

PC A61K48/00, A61P3/04, A61P9/00, A61P11/06, A61P13/00, A61P25/00, PC

A61P25/16,



PC A61P25/18,A61P25/20,A61P25/22,A61P31/04,A61P31/10,A61P31/12,  
 PC A61P31/18,  
 PC A61P35/00,A61P37/00,C07K14/705,C12N5/10,C12P21/02,C12Q1/02, PC  
 G01N33/53,  
 PC G01N33/566//C07K16/28,C12N15/00,A61K37/02,C12N5/00 CC  
 Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1. .1564  
 FT /organism='Unidentified'.

FEATURES Location/Qualifiers  
 source 1. .1564  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

# ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;  
 Best Local Similarity 99.9%; Pred. No. 2.6e-209;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	274	TACCCAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
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 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
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 Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
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 Db 814 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAAAGCGC 780  
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 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAAAGCGC 933

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
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 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
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 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
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 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
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 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233

Qy 1081 CTCAGTGG 1088  
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 Db 1234 CTCAGTGG 1241

# RESULT 10

E50811

LOCUS E50811 1564 bp DNA linear PAT 18-JUN-2001

DEFINITION Novel G protein-bound receptor (HFGAN 72X).

ACCESSION E50811

VERSION E50811.1 GI:13023198

KEYWORDS JP 2000060578-A/2.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 1564)

AUTHORS Derk, J.B. and Catharine, E.E.

TITLE Novel G protein-bound receptor (HFGAN 72X)

JOURNAL Patent: JP 2000060578-A 2 29-FEB-2000;

SMITHKLINE BEECHAM CORP

COMMENT OS Unidentified

PN JP 2000060578-A/2  
 PD 29-FEB-2000  
 PF 21-JUL-1999 JP 1999206115  
 PR 30-APR-1997 US 08/846704  
 PI DERK J BERGSMA, CATHARINE ELIZABETH ELLIS  
 PC C12N15/09, A61K31/70, A61K38/00, A61K39/00, A61K39/395, A61K39/395,  
 PC A61K45/00,  
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 A61P25/16,  
 PC A61P25/18, A61P25/20, A61P25/22, A61P31/04, A61P31/10, A61P31/12,  
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 G01N33/53,  
 PC G01N33/566//C07K16/28, C12N15/00, A61K37/02, C12N5/00 CC  
 Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1. .1564  
 FT /organism='Unidentified'.

FEATURES Location/Qualifiers  
 source 1. .1564  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

#### ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;  
 Best Local Similarity 99.9%; Pred. No. 2.6e-209;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC	573

Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1174	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1233
Qy	1081	CTCAGTGG	1088
Db	1234	CTCAGTGG	1241

RESULT 11

AX299473

LOCUS AX299473 1564 bp DNA linear PAT 26-NOV-2001

DEFINITION Sequence 1 from Patent EP1154019.

ACCESSION AX299473

VERSION AX299473.1 GI:17129230

KEYWORDS .

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1  
AUTHORS Bergsma, D.J. and Ellis, C.E.  
TITLE G-protein coupled receptor (hfgan72x)  
JOURNAL Patent: EP 1154019-A 1 14-NOV-2001;  
SmithKline Beecham Corporation (US)

## FEATURES

Location/Qualifiers  
source 1. .1564  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;  
Best Local Similarity 99.9%; Pred. No. 2.6e-209;  
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
      |||
Db     154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
      |||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
      |||
Db     274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
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Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753
Qy      601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
      |||
Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813
Qy      661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db      814 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873
Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780
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Db      874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 933
Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
      |||
Db      934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993
Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113
Qy      961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db      1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173
Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080
      |||
Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1233
Qy      1081 CTCAGTGG 1088
      |||
Db      1234 CTCAGTGG 1241

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# RESULT 12

AX299475

LOCUS AX299475 1564 bp DNA linear PAT 26-NOV-2001

DEFINITION Sequence 3 from Patent EP1154019.

ACCESSION AX299475

VERSION AX299475.1 GI:17129231

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Bergsma,D.J. and Ellis,C.E.

TITLE G-protein coupled receptor (hfgan72x)

JOURNAL Patent: EP 1154019-A 3 14-NOV-2001;

SmithKline Beecham Corporation (US)

FEATURES Location/Qualifiers

source 1. .1564  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;  
Best Local Similarity 99.9%; Pred. No. 2.6e-209;  
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
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Db      274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873
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Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
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Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
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Db	1114	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1174	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1233
Qy	1081	CTCAGTGG	1088
Db	1234	CTCAGTGG	1241

# RESULT 13

AX549082

LOCUS AX549082 1564 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 367 from Patent WO02061087.

ACCESSION AX549082

VERSION AX549082.1 GI:25813851

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.

TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides

JOURNAL Patent: WO 02061087-A 367 08-AUG-2002; Lifespan Biosciences, Inc. (US)

FEATURES Location/Qualifiers

source 1. .1564  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;  
Best Local Similarity 99.9%; Pred. No. 2.6e-209;



Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db     154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
      |||
Db     274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
      |||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
      |||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
      |||
Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
      |||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
      |||
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
      |||
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
      |||
Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
      |||
Db     814 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
      |||
Db     874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db     934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993
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Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
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 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
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 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 1114 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
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 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233  
 Qy 1081 CTCAGTGG 1088  
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 Db 1234 CTCAGTGG 1241

# RESULT 14

AX746121

LOCUS AX746121 1564 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 4 from Patent EP1156110.

ACCESSION AX746121

VERSION AX746121.1 GI:31744927

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Bergsma, D.J. and Ellis, C.E.

TITLE G-protein coupled receptor (HFGAN72Y)

JOURNAL Patent: EP 1156110-A 4 21-NOV-2001;

SMITHKLINE BEECHAM CORPORATION (US)

FEATURES Location/Qualifiers

source 1. .1564  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /note="HGS EST 554692"

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;  
 Best Local Similarity 99.9%; Pred. No. 2.6e-209;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60  
 |||  
 Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213  
 Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
 |||  
 Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
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 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233  
 Qy 1081 CTCAGTGG 1088  
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 Db 1234 CTCAGTGG 1241

# RESULT 15

AX840912

LOCUS AX840912 1564 bp DNA linear PAT 16-DEC-2003

DEFINITION Sequence 8 from Patent WO03075945.

ACCESSION AX840912

VERSION AX840912.1 GI:39979051

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Eulenberg, K., Steuernagel, A., Haeder, T. and Broenner, G.

TITLE Cg8327, cg10823, cg18418, cg15862, cg3768, cg11447 and cg16750  
 homologous proteins involved in the regulation of energy  
 homeostasis

JOURNAL Patent: WO 03075945-A 8 18-SEP-2003;

DeveloGen Aktiengesellschaft fuer entwicklungsbiologische;  
 Forschung (DE)

FEATURES

Location/Qualifiers

source

1. .1564

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;

Best Local Similarity 99.9%; Pred. No. 2.6e-209;

Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60  
 |||  
 Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213  
 Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
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 Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273  
 Qy 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180  
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 Db 274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333  
 Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
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Db 334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393  
 Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
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 Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453  
 Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG 360  
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 Db 454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG 513  
 Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573  
 Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
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 Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633  
 Qy 481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
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 Db 634 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693  
 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
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 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
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 Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
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 Db 814 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
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 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 933  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
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 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCTT 960  
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 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCTT 1113  
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 Db 1114 AAGAGGGTGTTCCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080  
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 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1233

Qy 1081 CTCAGTGG 1088  
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Db 1234 CTCAGTGG 1241

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Job time : 4593.56 secs

OM nucleic - nucleic search, using sw model

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Perfect score: 1133  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1133	100.0	1133	4	AAS00493	Aas00493 Human neu
2	1131.4	99.9	1133	2	AAT42828	Aat42828 Neuropept
3	1131.4	99.9	1133	2	AAV68512	Aav68512 Nucleotid
4	1131.4	99.9	1133	6	ABA96020	Aba96020 HGS EST 5
5	1128.2	99.6	1170	2	AAV68511	Aav68511 Nucleotid
6	1128.2	99.6	1170	6	ABA96019	Aba96019 G-protein
7	1086.4	95.9	1564	2	AAV63468	Aav63468 cDNA enco

8	1086.4	95.9	1564	2	AAV68514	Aav68514	Nucleotid
9	1086.4	95.9	1564	4	AAF32103	Aaf32103	Human HFG
10	1086.4	95.9	1564	6	ABA96021	Aba96021	HGS EST 5
11	1086.4	95.9	1564	6	AAI64173	Aai64173	HFGAN72X
12	1086.4	95.9	1564	6	AAI64172	Aai64172	Human HFG
13	1086.4	95.9	1564	7	ABZ42789	Abz42789	Human ore
14	1084.8	95.7	1110	2	AAT42827	Aat42827	Neuropept
15	1084.8	95.7	1278	4	AAS00491	Aas00491	Human neu
16	1084.8	95.7	1564	4	AAS17464	Aas17464	Human G p
17	1083.2	95.6	1209	2	AAT42826	Aat42826	Neuropept
18	1081.6	95.5	1278	5	ABI98014	Abi98014	Non-endog
19	1076.8	95.0	1110	4	AAS00492	Aas00492	Human neu
20	1040	91.8	1278	4	AAD09335	Aad09335	Cynomolgo
21	912	80.5	1281	5	AAC85974	Aac85974	Dog orexi
22	670.6	59.2	789	2	AAT13909	Aat13909	Rabbit G-
23	670.6	59.2	789	2	AAT51065	Aat51065	G-protein
24	520.8	46.0	1633	2	AAX29700	Aax29700	Human 7-t
25	520.8	46.0	1843	7	ABZ42790	Abz42790	Human ore
26	516.2	45.6	1335	4	AAF90300	Aaf90300	Nucleotid
27	516	45.5	1335	5	ABI98015	Abi98015	Non-endog
28	249.2	22.0	344	5	AAF56748	Aaf56748	Human HCR
29	249.2	22.0	9785	5	AAF55159	Aaf55159	Nucleotid
30	249.2	22.0	10453	4	AAS17462	Aas17462	Human G p
31	244	21.5	244	4	AAS17449	Aas17449	Human G p
32	230	20.3	331	5	AAF56750	Aaf56750	Human HCR
33	225.4	19.9	227	4	AAS17453	Aas17453	Human G p
34	197.4	17.4	356	4	AAS17445	Aas17445	Human G p
35	197	17.4	452	5	AAF56746	Aaf56746	Human HCR
36	181	16.0	263	5	AAF56747	Aaf56747	Human HCR
37	179	15.8	179	4	AAS17447	Aas17447	Human G p
38	163.2	14.4	1290	3	AAA70507	Aaa70507	Novel hum
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# ALIGNMENTS

## RESULT 1

AAS00493

ID AAS00493 standard; cDNA; 1133 BP

XX

AC AAS00493;

XX

DT 17-MAY-2001 (first entry)

XX

DE Human neuropeptide receptor splice variant 2 cDNA.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;

KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;

KW cardiovascular disorder; autoimmune disorder; infectious disorder;

KW eating behaviour disorder; narcolepsy; neurological disease;



KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;  
 KW protein co-ordinate data; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1. .1119  
 FT /\*tag= a  
 FT /product= "neuropeptide receptor splice variant 2"  
 XX  
 PN WO200117532-A1.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 07-SEP-2000; 2000WO-US024518.  
 XX  
 PR 10-SEP-1999; 99US-00393696.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Soppet DR, Li Y, Rosen CA;  
 XX  
 DR WPI; 2001-183276/18.  
 DR P-PSDB; AAU00440.  
 XX  
 PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,  
 PT useful for preventing, treating or ameliorating obesity, narcolepsy,  
 PT neurological disease and addiction to narcotics, nicotine and alcohol.  
 XX  
 PS Claim 4; Fig 3; 385pp; English.  
 XX  
 CC The present sequence encodes for human neuropeptide receptor splice  
 CC variant 2. Two splice variants (AAU00439-AAU00440) and a possible mutant  
 CC (AAU00442) of a novel human neuropeptide receptor (AAU00438) are  
 CC described. The neuropeptide receptor shows sequence homology to the  
 CC neuropeptide Y receptor. Polypeptides and polynucleotides of the  
 CC neuropeptide receptor are useful for diagnosing, preventing, or treating  
 CC a pathological condition in a subject related to the central nervous and  
 CC peripheral nervous systems (CNS and PNS). The polypeptides and  
 CC polynucleotides may be used to treat hyperproliferative, cardiovascular,  
 CC autoimmune, nervous system or infectious disorders e.g. cancer, heart  
 CC disease, rheumatoid arthritis, Alzheimer's disease, HIV infection and  
 CC diabetes mellitus. In particular they are useful for preventing, treating  
 CC or ameliorating a medical condition in a mammal such as obesity/eating  
 CC behaviour disorders, narcolepsy, neurological disease, addiction to  
 CC narcotics, nicotine and alcohol, chronic pain, acute pain, migraine  
 CC headaches and anxiety disorders. The polynucleotides encoding the  
 CC neuropeptide receptor can also be used in gene therapy methods for  
 CC treating such diseases  
 XX  
 SQ Sequence 1133 BP; 202 A; 367 C; 313 G; 251 T; 0 U; 0 Other;  
  
 Query Match 100.0%; Score 1133; DB 4; Length 1133;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-263;  
 Matches 1133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCCC 60

Db	1		ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Qy	61		TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61		TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121		TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC	180
Db	121		TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC	180
Qy	181		CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181		CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241		ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241		ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301		CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCTGGCCATGCCCTCTGCAAG	360
Db	301		CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCTGGCCATGCCCTCTGCAAG	360
Qy	361		GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361		GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661		ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661		ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900

```

Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
        |||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
Qy      961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
        |||
Db      961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
        |||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
Qy      1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133
        |||
Db      1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133

```

# RESULT 2

AAT42828

ID AAT42828 standard; cDNA; 1133 BP.

XX

AC AAT42828;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor splice variant-2 gene.

XX

KW Human; neuropeptide receptor; splice variant; drug screening;

KW receptor-agonist; receptor-antagonist; anorectic; antitumour;

KW anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;

KW sedative; diagnostic; gene therapy; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	misc_feature	1117. .1119
----	--------------	-------------

FT		/*tag= a
----	--	----------

FT		/note= "In-frame stop codon"
----	--	------------------------------

XX

PN WO9634877-A1.

XX

PD 07-NOV-1996.

XX

PF 05-MAY-1995; 95WO-US005616.

XX

PR 05-MAY-1995; 95WO-US005616.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Soppet DR, Li Y, Rosen CA;

XX

DR WPI; 1996-506094/50.

DR P-PSDB; AAW06126.

XX

PT Human neuro-peptide receptor polypeptide(s) - used to identify

PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of  
PT obesity, Alzheimer's disease, epilepsy, etc. .

XX

PS Disclosure; Page 52; 77pp; English.

XX

CC The sequence encodes human neuropeptide receptor splice variant-2, which  
CC retains activity corresponding to the mature receptor (encoded by  
CC AAT42826). The receptor gene has been isolated from from a human adult  
CC hypothalamus cDNA library, and is structurally related to the G-protein-  
CC coupled receptor family. The receptor may be used in a drug screening  
CC assay for isolation of receptor-agonists and -antagonists, which may be  
CC used as anorectic, antitumour, anticholesterolemic, neuroprotective,  
CC anticonvulsant, hypotensive or sedative drugs, etc. The DNA may also be  
CC used in genetic disease diagnosis or gene therapy. The receptor and its  
CC corresponding antibody may also be used in therapy and diagnosis

XX

SQ Sequence 1133 BP; 202 A; 368 C; 312 G; 251 T; 0 U; 0 Other;

Query Match 99.9%; Score 1131.4; DB 2; Length 1133;

Best Local Similarity 99.9%; Pred. No. 4.5e-263;

Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGACCCC	60
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540

Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961	AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Qy	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG	1133
Db	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG	1133

# RESULT 3

AAV68512

ID AAV68512 standard; cDNA; 1133 BP.

XX

AC AAV68512;

XX

DT 29-JAN-1999 (first entry)

XX

DE Nucleotide sequence of HGS EST 557082.

XX

KW HGS EST 557082; G-protein coupled receptor family; HFGAN72Y; mutation;

KW probe; agonist; antagonist; activation; inhibition; gene therapy;

KW antibody; immune response; vaccine; HIV-1; HIV-2; cancer; anorexia;

KW bulimia; asthma; Parkinson's disease; acute heart failure; hypotension;

KW hypertension; urinary retention; osteoporosis; angina pectoris;

KW myocardial infarction; ulcer; allergies; psychotic disorder;  
KW neurological disorder; gene mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP875565-A2.  
XX  
PD 04-NOV-1998.  
XX  
PF 27-OCT-1997; 97EP-00308554.  
XX  
PR 30-APR-1997; 97US-00846705.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Bergsma DJ, Ellis C;  
XX  
DR WPI; 1998-570286/49.  
XX  
PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -  
PT useful as diagnostic reagents and for prevention and treatment of HIV  
PT infections, cancer, osteoporosis and Parkinson's disease.  
XX  
PS Example 1; Page 18-19; 22pp; English.  
XX  
CC This is the nucleotide sequence of the HGS EST 557082 used in the method  
CC of the invention involving the G-protein coupled receptor, HFGAN72Y. Its  
CC polypeptides and polynucleotides are useful for diagnosing susceptibility  
CC to diseases by detecting mutations in the HFGAN72Y gene using probes  
CC containing the HFGAN72Y nucleotide sequence, and can diagnose diseases  
CC associated with HFGAN72Y imbalance by determining HFGAN72Y polypeptide or  
CC mRNA expression levels. Agonists/antagonists can be used in treatment to  
CC activate/inhibit HFGAN72Y activity, in addition to direct administration  
CC of antisense sequences to prevent expression, or HFGAN72Y polypeptides to  
CC treat conditions associated with a lack HFGAN72Y protein. Gene therapy  
CC may also be used to affect endogenous HFGAN72Y polypeptide production.  
CC HFGAN72Y antibodies are useful for inducing an immune response to  
CC immunise and prevent diseases, and for isolating HFGAN72Y clones or  
CC purifying the polypeptides by affinity chromatography. HFGAN72Y  
CC polypeptides can be administered directly or as a vaccine to inoculate  
CC against diseases. Diseases diagnosed, prevented or treated include HIV-1  
CC or HIV-2 infections, pain, cancers, anorexia, bulimia, asthma,  
CC Parkinson's disease, acute heart failure, hypotension, hypertension,  
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,  
CC ulcers; allergies, benign prostatic hypertrophy, and psychotic and  
CC neurological disorders. The HFGAN72Y polypeptide is also useful for  
CC mapping the gene to a chromosome, allowing gene inheritance to be studied  
CC through linkage analysis.  
XX  
SQ Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

Query Match 99.9%; Score 1131.4; DB 2; Length 1133;  
Best Local Similarity 99.9%; Pred. No. 4.5e-263;  
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCCC 60  
|||||

Db	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	60
Qy	61	TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	61	TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Db	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133  
 |||  
 Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133

RESULT 4

ABA96020

ID ABA96020 standard; cDNA; 1133 BP.

XX

AC ABA96020;

XX

DT 12-MAR-2002 (first entry)

XX

DE HGS EST 557082.

XX

KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;  
 KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;  
 KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;  
 KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;  
 KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;  
 KW schizophrenia; manic depression; dementia; mental retardation; EST;  
 KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;  
 KW HGS EST 557082; expressed sequence tag; ss.

XX

OS Homo sapiens.

XX

PN EP1156110-A2.

XX

PD 21-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203010.

XX

PR 30-APR-1997; 97US-00845705.

PR

27-OCT-1997; 97EP-00308554.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-084320/12.

XX

PT New polynucleotide encoding a G-protein coupled receptor designated  
 PT HFGAN72Y is useful to diagnose and treat associated diseases including  
 PT cancer, infection, cardiac disease and psychotic and neurological



PT disorders.

XX

PS Example 1; Page 18-19; 22pp; English.

XX

CC The sequence represents HGS EST 557082. The invention relates to a novel  
CC isolated polynucleotide encoding HFGAN72Y polypeptide. The polypeptide of  
CC the invention has cytostatic, cardiant, analgesic, tranquillising,  
CC nootropic, neuroprotective, and anti-asthmatic activity. The HFGAN72Y has  
CC a use in gene therapy. The HFGAN72Y polynucleotide or an HFGAN72Y  
CC polypeptide agonist are used to treat a subject in need of enhanced  
CC HFGAN72Y activity or expression. An HFGAN72Y antagonist or competitor, or  
CC nucleic acid which inhibits HFGAN72Y expression is used to treat a  
CC subject in need of decreased HFGAN72Y activity or expression. HFGAN72Y-  
CC associated diseases include infections, particularly by HIV-1 or HIV-2,  
CC pain, anorexia, bulimia, Parkinson's disease, cardiac diseases, cancers,  
CC ulcers, urinary retention, asthma, allergies, benign prostatic  
CC hypertrophy, and psychotic and neurological disorders including anxiety,  
CC schizophrenia, manic depression, delirium, dementia, severe mental  
CC retardation and dyskinesias such as Huntington's disease and Tourette's  
CC syndrome

XX

SQ Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

Query Match 99.9%; Score 1131.4; DB 6; Length 1133;  
Best Local Similarity 99.9%; Pred. No. 4.5e-263;  
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCTGCTGGCCATCATGGTGGCCAGGCT	540
Db	481		540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541		600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601		660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661		720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAAAGCGC	780
Db	721		780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781		840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841		900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901		960
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961		1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1021		1080
Qy	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG	1133
Db	1081		1133

RESULT 5

AAV68511

ID AAV68511 standard; cDNA; 1170 BP.

XX

AC AAV68511;

XX

DT 29-JAN-1999 (first entry)

XX

DE Nucleotide sequence of HFGAN72Y a G-protein coupled receptor.

XX

KW G-protein coupled receptor family; HFGAN72Y; mutation; probe; agonist;  
KW antagonist; activation; inhibition; gene therapy; antibody;  
KW immune response; vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia;  
KW asthma; Parkinson's disease; acute heart failure; hypotension;  
KW hypertension; urinary retention; osteoporosis; angina pectoris;  
KW myocardial infarction; ulcer; allergies; psychotic disorder;  
KW neurological disorder; gene mapping; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	1. .1170
FT		/*tag= a
FT		/product= "HFGAN72Y protein"

XX

PN EP875565-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308554.

XX

PR 30-APR-1997; 97US-00846705.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis C;

XX

DR WPI; 1998-570286/49.

DR P-PSDB; AAW80805.

XX

PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -  
PT useful as diagnostic reagents and for prevention and treatment of HIV  
PT infections, cancer, osteoporosis and Parkinson's disease.

XX

PS Claim 3; Page 7; 22pp; English.

XX

CC This is the nucleotide sequence of the G-protein coupled receptor,  
CC HFGAN72Y used in the method of the invention. HFGAN72Y polypeptides and  
CC polynucleotides are useful for diagnosing susceptibility to diseases by  
CC detecting mutations in the HFGAN72Y gene using probes containing the  
CC HFGAN72Y nucleotide sequence, and can diagnose diseases associated with  
CC HFGAN72Y imbalance by determining HFGAN72Y polypeptide or mRNA expression  
CC levels. Agonists/antagonists can be used in treatment to activate/inhibit  
CC HFGAN72Y activity, in addition to direct administration of antisense  
CC sequences to prevent expression, or HFGAN72Y polypeptides to treat  
CC conditions associated with a lack HFGAN72Y protein. Gene therapy may also  
CC be used to affect endogenous HFGAN72Y polypeptide production. HFGAN72Y  
CC antibodies are useful for inducing an immune response to immunise and  
CC prevent diseases, and for isolating HFGAN72Y clones or purifying the  
CC polypeptides by affinity chromatography. HFGAN72Y polypeptides can be  
CC administered directly or as a vaccine to inoculate against diseases.  
CC Diseases diagnosed, prevented or treated include HIV-1 or HIV-2  
CC infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's  
CC disease, acute heart failure, hypotension, hypertension, urinary  
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcers;  
CC allergies, benign prostatic hypertrophy, and psychotic and neurological  
CC disorders. The HFGAN72Y polypeptide is also useful for mapping the gene

CC to a chromosome, allowing gene inheritance to be studied through linkage  
CC analysis  
XX  
SQ Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

Query Match 99.6%; Score 1128.2; DB 2; Length 1170;  
Best Local Similarity 99.7%; Pred. No. 2.7e-262;  
Matches 1130; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCTGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCTGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
```

Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961	AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Qy	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCTGACCATCGTGCCCCGG	1133
Db	1081	CTCAGTGGATGTAAAGAGAAGAGTCTAGCTCTGTCTGCCCATCGTGCCCCGG	1133

# RESULT 6

ABA96019

ID ABA96019 standard; cDNA; 1170 BP.

XX

AC ABA96019;

XX

DT 12-MAR-2002 (first entry)

XX

DE G-protein coupled receptor (HFGAN72Y) cDNA.

XX

KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;  
 KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;  
 KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;  
 KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;  
 KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;  
 KW schizophrenia; manic depression; dementia; mental retardation;  
 KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .1170

FT /\*tag= a

FT /product= "HGFAN72Y"

XX

PN EP1156110-A2.

XX

PD 21-NOV-2001.

XX  
PF 27-OCT-1997; 2001EP-00203010.  
XX  
PR 30-APR-1997; 97US-00846705.  
PR 27-OCT-1997; 97EP-00308554.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.

Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCTT	960
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCTGCTTC	1020
Db	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCTGCTTC	1020
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT	1080
Db	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT	1080

QY 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCTGACCATCGTGCCCCGG 1133  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGCTCTGTCTGCCCCATCGTGCCCCGG 1133

RESULT 7

AAV63468

ID AAV63468 standard; cDNA; 1564 BP.

XX

AC AAV63468;

XX

DT 26-JAN-1999 (first entry)

XX

DE cDNA encoding G-protein coupled receptor (HFGAN72X) polypeptide.

XX

KW G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;

KW bulimia; asthma; Parkinson's disease; acute heart failure;

KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;

KW benign prostatic hypertrophy; neurological disorder; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 154..1431

FT /\*tag= a

FT /product= "HFGAN72X"

XX

PN EP875566-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308563.

XX

PR 30-APR-1997; 97US-00846704.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 1998-559432/48.

DR P-PSDB; AAW80456.

XX

PT New human G-protein coupled receptor HFGAN72X polypeptide and

PT polynucleotide - useful as diagnostic reagents and for treating e.g. HIV

PT infection, cancer and Parkinson's disease.

XX

PS Claim 3; Page 7; 24pp; English.

XX

CC The present sequence encodes a G-protein coupled receptor (HFGAN72X)

CC polypeptide. HFGAN72X polypeptides and polynucleotides are useful for

CC diagnosing diseases related to over or under expression of HFGAN72X

CC proteins by identifying mutations in the HFGAN72X gene using HFGAN72X

CC probes, or determining HFGAN72X protein or mRNA expression levels.

CC HFGAN72X polypeptides are also useful for screening for compounds which

CC affect activity of the protein. Diseases that can be treated with

CC HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,



CC asthma, Parkinson's disease, acute heart failure, hypotension,  
CC hypertension, urinary retention, osteoporosis, angina pectoris,  
CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,  
CC and psychotic and neurological disorders

XX

SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 95.9%; Score 1086.4; DB 2; Length 1564;  
Best Local Similarity 99.9%; Pred. No. 3.6e-252;  
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGCTAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGCTAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCAGATATTCCGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db 814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGGGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGGGAAGCGC 933

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1233

Qy 1081 CTCAGTGG 1088  
 |||||||

Db 1234 CTCAGTGG 1241

RESULT 8

AAV68514

ID AAV68514 standard; cDNA; 1564 BP.

XX

AC AAV68514;

XX

DT 29-JAN-1999 (first entry)

XX

DE Nucleotide sequence of a probe HGS EST 554692.

XX

KW Probe HGS EST 554692; G-protein coupled receptor family; HFGAN72Y;

KW mutation; probe; agonist; antagonist; activation; inhibition;

KW gene therapy; antibody; immune response; vaccine; HIV-1; HIV-2; cancer;

KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;

KW hypotension; hypertension; urinary retention; osteoporosis;

KW angina pectoris; myocardial infarction; ulcer; allergies;

KW psychotic disorder; neurological disorder; gene mapping; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN EP875565-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308554.

XX  
 PR 30-APR-1997; 97US-00846705.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Bergsma DJ, Ellis C;  
 XX  
 DR WPI; 1998-570286/49.  
 XX  
 PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -  
 PT useful as diagnostic reagents and for prevention and treatment of HIV  
 PT infections, cancer, osteoporosis and Parkinson's disease.  
 XX  
 PS Example 1; Page 19-20; 22pp; English.  
 XX

CC This is the nucleotide sequence of the probe HGS EST 554692 used in the  
 CC method of the invention involving the G-protein coupled receptor,  
 CC HFGAN72Y. Its polypeptides and polynucleotides are useful for diagnosing  
 CC susceptibility to diseases by detecting mutations in the HFGAN72Y gene  
 CC using probes containing the HFGAN72Y nucleotide sequence, and can  
 CC diagnose diseases associated with HFGAN72Y imbalance by determining  
 CC HFGAN72Y polypeptide or mRNA expression levels. Agonists/antagonists can  
 CC be used in treatment to activate/inhibit HFGAN72Y activity, in addition  
 CC to direct administration of antisense sequences to prevent expression, or  
 CC HFGAN72Y polypeptides to treat conditions associated with a lack HFGAN72Y  
 CC protein. Gene therapy may also be used to affect endogenous HFGAN72Y  
 CC polypeptide production. HFGAN72Y antibodies are useful for inducing an  
 CC immune response to immunise and prevent diseases, and for isolating  
 CC HFGAN72Y clones or purifying the polypeptides by affinity chromatography.  
 CC HFGAN72Y polypeptides can be administered directly or as a vaccine to  
 CC inoculate against diseases. Diseases diagnosed, prevented or treated  
 CC include HIV-1 or HIV-2 infections, pain, cancers, anorexia, bulimia,  
 CC asthma, Parkinson's disease, acute heart failure, hypotension,  
 CC hypertension, urinary retention, osteoporosis, angina pectoris,  
 CC myocardial infarction, ulcers; allergies, benign prostatic hypertrophy,  
 CC and psychotic and neurological disorders. The HFGAN72Y polypeptide is  
 CC also useful for mapping the gene to a chromosome, allowing gene  
 CC inheritance to be studied through linkage analysis  
 XX

SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 95.9%; Score 1086.4; DB 2; Length 1564;  
 Best Local Similarity 99.9%; Pred. No. 3.6e-252;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGCCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC	333

Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC	1080

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC 1233

Qy      1081 CTCAGTGG 1088
      |||||||
Db      1234 CTCAGTGG 1241

```

RESULT 9

AAF32103

ID AAF32103 standard; cDNA; 1564 BP.

XX

AC AAF32103;

XX

DT 10-APR-2001 (first entry)

XX

DE Human HFGAN72 receptor coding sequence SEQ ID NO: 12.

XX

KW Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;

KW truncation mutant; ligand; neurodegenerative disorder; pain;

KW eating disorder; behaviour disorder; mood disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200100787-A2.

XX

PD 04-JAN-2001.

XX

PF 22-JUN-2000; 2000WO-US017251.

XX

PR 25-JUN-1999; 99US-0141156P.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;

XX

DR WPI; 2001-071483/08.

XX

PT Polynucleotides encoding Lig 72A polypeptides or their variants, which

PT are useful in the treatment of a disease or disorder associated with

PT pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,

PT neuropathic pain and back pain.

XX

PS Disclosure; Fig 6; 101pp; English.

XX

CC The present invention provides the protein and coding sequences for the

CC human, mouse and rat HFGAN receptor ligand Lig72A. It also provides

CC truncated mutant versions. These, and their agonists and antagonists, are

CC all useful in the treatment of eating, neurodegenerative, behaviour,

CC mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy

CC and acute inflammatory conditions

XX

SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 95.9%; Score 1086.4; DB 4; Length 1564;

Best Local Similarity 99.9%; Pred. No. 3.6e-252;

Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
      |||
Db     154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
      |||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
      |||
Db     274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
      |||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
      |||
Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
      |||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
      |||
Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
      |||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
      |||
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
      |||
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
      |||
Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
      |||
Db     814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy     721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780
      |||
Db     874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 933

Qy     781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
      |||
Db     934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993
```

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG .900  
 |||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233  
 Qy 1081 CTCAGTGG 1088  
 |||  
 Db 1234 CTCAGTGG 1241

RESULT 10

ABA96021

ID ABA96021 standard; cDNA; 1564 BP.

XX

AC ABA96021;

XX

DT 12-MAR-2002 (first entry)

XX

DE HGS EST 554692.

XX

KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;  
 KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;  
 KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;  
 KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;  
 KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;  
 KW schizophrenia; manic depression; dementia; mental retardation; EST;  
 KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;  
 KW HGS EST 554692; expressed sequence tag; probe; ss.

XX

OS Homo sapiens.

XX

PN EP1156110-A2.

XX

PD 21-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203010.

XX

PR 30-APR-1997; 97US-00846705.

PR 27-OCT-1997; 97EP-00308554.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-084320/12.

XX  
PT New polynucleotide encoding a G-protein coupled receptor designated  
PT HFGAN72Y is useful to diagnose and treat associated diseases including  
PT cancer, infection, cardiac disease and psychotic and neurological  
PT disorders.  
XX  
PS Example 1; Page 19-20; 22pp; English.  
XX  
CC The sequence represents HGS EST 554692. The sequence was used in the  
CC invention as a probe to screen a human genomic placenta phage library.  
CC The invention relates to a novel isolated polynucleotide encoding  
CC HFGAN72Y polypeptide. The polypeptide of the invention has cytostatic,  
CC cardiant, analgesic, tranquillising, nootropic, neuroprotective, and anti  
CC -asthmatic activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y  
CC polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a  
CC subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y  
CC antagonist or competitor, or nucleic acid which inhibits HFGAN72Y  
CC expression is used to treat a subject in need of decreased HFGAN72Y  
CC activity or expression. HFGAN72Y-associated diseases include infections,  
CC particularly by HIV-1 or HIV-2, pain, anorexia, bulimia, Parkinson's  
CC disease, cardiac diseases, cancers, ulcers, urinary retention, asthma,  
CC allergies, benign prostatic hypertrophy, and psychotic and neurological  
CC disorders including anxiety, schizophrenia, manic depression, delirium,  
CC dementia, severe mental retardation and dyskinesias such as Huntington's  
CC disease and Tourette's syndrome  
XX  
SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;  
Best Local Similarity 99.9%; Pred. No. 3.6e-252;  
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60  
|||||  
Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213  
Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
|||||  
Db 214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273  
Qy 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180  
|||||  
Db 274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333  
Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
|||||  
Db 334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393  
Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
|||||  
Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453  
Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
|||||  
Db 454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513  
Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420



Db	514		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481		GGCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634		GGCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC	1020
Db	1114		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1080
Db	1174		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1233
Qy	1081		CTCAGTGG	1088
Db	1234		CTCAGTGG	1241

RESULT 11

AAI64173

ID AAI64173 standard; cDNA; 1564 BP.

XX

AC AAI64173;

XX  
 DT 22-JAN-2002 (first entry)  
 XX  
 DE HFGAN72X G coupled receptor polypeptide partial sequence.  
 XX  
 KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;  
 KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;  
 KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;  
 KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;  
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;  
 KW urinary retention; osteoporosis; angina pectoris; probe;  
 KW myocardial infarction; ulcers; asthma; allergy; delirium; dementia;  
 KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;  
 KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 154..1362  
 FT /\*tag= a  
 FT /partial  
 FT /product= "HFGAN72X protein"  
 FT /note= "The specification states that this is a partial  
 FT sequence even though it contains start and stop codons;  
 FT HFGAN72X is a G coupled receptor polypeptide"  
 FT /transl\_except= (pos:991..993, aa:Ala)  
 XX  
 PN EP1154019-A2.  
 XX  
 PD 14-NOV-2001.  
 XX  
 PF 27-OCT-1997; 2001EP-00203008.  
 XX  
 PR 30-APR-1997; 97US-00846704.  
 PR 27-OCT-1997; 97EP-00308563.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Bergsma DJ, Ellis CE;  
 XX  
 DR WPI; 2002-012659/02.  
 DR P-PSDB; AAG78346.  
 XX  
 PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and  
 PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's  
 PT disease, and acute heart failure.  
 XX  
 PS Example 3; Page 9; 24pp; English.  
 XX  
 CC The present sequence is that of a known partial nucleotide sequence  
 CC encoding a HFGAN72X polypeptide (AAG78346) used as a probe to identify  
 CC the HFGAN72X gene (AAI64173). The specification describes a newly  
 CC isolated polynucleotide encoding a human HFGAN72X G coupled receptor  
 CC polypeptide. The protein of the invention has antibacterial, fungicide,  
 CC virucide, protozoacide, anti-HIV, cardiant, analgesic, cytostatic,  
 CC nootropic, antiparkinsonian, antiulcer, antiasthmatic, tranquiliser,  
 CC neuroleptic, antidepressant, anticonvulsant and osteopathic activities.

CC HFGAN72X polynucleotides (PNs) are used to express HFGAN72X in vivo, to  
 CC treat diseases requiring increased activity or expression of HFGAN72X;  
 CC for recombinant production of HFGAN72X; diagnose diseases by detecting  
 CC mutations in genomic sequences and in chromosome identification and  
 CC mapping. HFGAN72X polypeptides are used to raise specific antibodies; as  
 CC therapeutic agents; to identify HFGAN72X protein-expressing clones; to  
 CC purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X  
 CC PNs are used to identify (ant)agonists of HFGAN72X, useful  
 CC therapeutically. Nucleic acids that inhibit expression of HFGAN72X and  
 CC polypeptides that compete with ligands for binding to HFGAN72X proteins  
 CC are also useful therapeutically and diagnostically. HFGAN72X-related  
 CC diseases include infections (bacterial, viral, fungal or protozoal,  
 CC particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's  
 CC disease; acute heart failure; hypotension; hypertension; urinary  
 CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;  
 CC asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;  
 CC manic depression; delirium; dementia; severe mental retardation and  
 CC dyskinesias

XX

SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;  
 Best Local Similarity 99.9%; Pred. No. 3.6e-252;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	274	TACCCAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGATCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGATCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633

Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1174	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1233
Qy	1081	CTCAGTGG	1088
Db	1234	CTCAGTGG	1241

RESULT 12

AAI64172

ID AAI64172 standard; cDNA; 1564 BP.

XX

AC AAI64172;

XX

DT 22-JAN-2002 (first entry)

XX

DE Human HFGAN72X G coupled receptor polypeptide cDNA.

XX

KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;  
 KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;

KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;  
 KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;  
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;  
 KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;  
 KW ulcers; asthma; allergy; delirium; dementia;  
 KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;  
 KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 154..1431  
 FT /\*tag= a  
 FT /product= "HFGAN72X protein"  
 FT /note= "G coupled receptor polypeptide"  
 XX  
 PN EP1154019-A2.  
 XX  
 PD 14-NOV-2001.  
 XX  
 PF 27-OCT-1997; 2001EP-00203008.  
 XX  
 PR 30-APR-1997; 97US-00846704.  
 PR 27-OCT-1997; 97EP-00308563.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Bergsma DJ, Ellis CE;  
 XX  
 DR WPI; 2002-012659/02.  
 DR P-PSDB; AAG78345.  
 XX  
 PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and  
 PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's  
 PT disease, and acute heart failure.  
 XX  
 PS Claim 3; Page 7; 24pp; English.  
 XX  
 CC The present sequence is that of a cDNA encoding a HFGAN72X polypeptide  
 CC (AAG78345). The specification describes a newly isolated polynucleotide  
 CC encoding a HFGAN72X G coupled receptor polypeptide. The protein of the  
 CC invention has antibacterial, fungicide, virucide, protozoacide, anti-HIV,  
 CC cardiant, analgesic, cytostatic, nootropic, antiparkinsonian, antiulcer,  
 CC antiasthmatic, tranquiliser, neuroleptic, antidepressant, anticonvulsant  
 CC and osteopathic activities. HFGAN72X polynucleotides (PNs) are used to  
 CC express HFGAN72X in vivo, to treat diseases requiring increased activity  
 CC or expression of HFGAN72X; for recombinant production of HFGAN72X;  
 CC diagnose diseases (or susceptibility to them) by detecting mutations in  
 CC genomic sequences and in chromosome identification and mapping. HFGAN72X  
 CC polypeptides are used to raise specific antibodies; as therapeutic agents  
 CC ; to identify HFGAN72X protein-expressing clones; to purify HFGAN72X  
 CC proteins; in vaccines. Cells transformed with HFGAN72X PNs are used to  
 CC identify (ant)agonists of HFGAN72X, useful therapeutically. Nucleic acids  
 CC that inhibit expression of HFGAN72X and polypeptides that compete with  
 CC ligands for binding to HFGAN72X proteins are also useful therapeutically  
 CC and diagnostically. HFGAN72X-related diseases include infections  
 CC (bacterial, viral, fungal or protozoal, particularly HIV-1 or -2); pain;

CC cancer; anorexia; bulimia; Parkinson's disease; acute heart failure;  
CC hypotension; hypertension; urinary retention; osteoporosis; angina  
CC pectoris; myocardial infarction; ulcers; asthma; allergy; benign  
CC prostatic hypertrophy; anxiety; schizophrenia; manic depression; delirium  
CC ; dementia; severe mental retardation and dyskinesias  
XX  
SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 95.9%; Score 1086.4; DB 6; Length 1564;  
Best Local Similarity 99.9%; Pred. No. 3.6e-252;  
Matches 1087; Conservatiye 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy     421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy     481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693

Qy     541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy     601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy     661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
```

Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	1114	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1174	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1233
Qy	1081	CTCAGTGG	1088
Db	1234	CTCAGTGG	1241

RESULT 13

ABZ42789

ID ABZ42789 standard; DNA; 1564 BP.

XX

AC ABZ42789;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human orexin receptor 1 nucleotide SEQ ID NO:367.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KW ulcer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX  
 PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US050107.  
 XX  
 PR 19-DEC-2000; 2000US-0257144P.  
 XX  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 PI Burmer GC, Roush CL, Brown JP;  
 XX  
 DR WPI; 2003-046718/04.  
 DR P-PSDB; ABP81941.  
 XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Fig 1; 523pp; English.  
 XX  
 CC The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 1564 BP; 268 A; 513 C; 436 G; 347 T; 0 U; 0 Other;

Query Match 95.9%; Score 1086.4; DB 7; Length 1564;  
 Best Local Similarity 99.9%; Pred. No. 3.6e-252;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213



Qy	61	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	180
Db	274	TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGTACCTGCCCATCAGCGTCCTCAATGTCCTT	960

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113
Qy      961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173
Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233
Qy      1081 CTCAGTGG 1088
      ||||||||
Db      1234 CTCAGTGG 1241

```

RESULT 14

AAT42827

ID AAT42827 standard; cDNA; 1110 BP.

XX

AC AAT42827;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor splice variant-1 gene.

XX

KW Human; neuropeptide receptor; splice variant; drug screening;  
 KW receptor-agonist; receptor-antagonist; anorectic; antitumour;  
 KW anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;  
 KW sedative; diagnostic; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN WO9634877-A1.

XX

PD 07-NOV-1996.

XX

PF 05-MAY-1995; 95WO-US005616.

XX

PR 05-MAY-1995; 95WO-US005616.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Soppet DR, Li Y, Rosen CA;

XX

DR WPI; 1996-506094/50.

DR

P-PSDB; AAW06125.

XX

PT Human neuro-peptide receptor polypeptide(s) - used to identify  
 PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of  
 PT obesity, Alzheimer's disease, epilepsy, etc.

XX

PS Disclosure; Page 50-51; 77pp; English.

XX

CC The sequence encodes human neuropeptide receptor splice variant-1, which  
 CC retains activity corresponding to the mature receptor (encoded by  
 CC AAT42826). The receptor gene has been isolated from from a human adult

CC hypothalamus cDNA library, and is structurally related to the G-protein-  
CC coupled receptor family. The receptor may be used in a drug screening..  
CC assay for isolation of receptor-agonists and -antagonists, which may be  
CC used as anorectic, antitumour, anticholesterolemic, neuroprotective,  
CC anticonvulsant, hypotensive or sedative drugs, etc. The DNA may also be  
CC used in genetic disease diagnosis or gene therapy. The receptor and its  
CC corresponding antibody may also be used in therapy and diagnosis

XX

SQ Sequence 1110 BP; 194 A; 364 C; 305 G; 247 T; 0 U; 0 Other;

Query Match 95.7%; Score 1084.8; DB 2; Length 1110;  
Best Local Similarity 99.8%; Pred. No. 7.9e-252;  
Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
      |||
Db      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780
      |||
Db      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
      |||
Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
      |||
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
      |||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC 1020
      |||
Db      961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080
      |||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC 1080

Qy      1081 CTCAGTGG 1088
      |||
Db      1081 CTCAGTGG 1088

```

# RESULT 15

AAS00491

ID AAS00491 standard; cDNA; 1278 BP.

XX

AC AAS00491;

XX

DT 17-MAY-2001 (first entry)

XX

DE Human neuropeptide receptor cDNA.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;  
KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;  
KW cardiovascular disorder; autoimmune disorder; infectious disorder;  
KW eating behaviour disorder; narcolepsy; neurological disease;  
KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;  
KW protein co-ordinate data; chromosome 1; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .1278

FT /\*tag= a

FT /product= "neuropeptide receptor"

XX  
 PN WO200117532-A1.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 07-SEP-2000; 2000WO-US024518.  
 XX  
 PR 10-SEP-1999; 99US-00393696.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Soppet DR, Li Y, Rosen CA;  
 XX  
 DR WPI; 2001-183276/18.  
 DR P-PSDB; AAU00438.  
 XX  
 PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,  
 PT useful for preventing, treating or ameliorating obesity, narcolepsy,  
 PT neurological disease and addiction to narcotics, nicotine and alcohol.  
 XX  
 PS Claim 4; Fig 1; 385pp; English.  
 XX  
 CC The present sequence encodes for a novel human neuropeptide receptor  
 CC which shows sequence homology to the neuropeptide Y receptor. Two splice  
 CC variants of the neuropeptide receptor (AAU00439-AAU00440) and a possible  
 CC mutant (AAU00442) are also described. Polypeptides and polynucleotides of  
 CC the neuropeptide receptor are useful for diagnosing, preventing, or  
 CC treating a pathological condition in a subject related to the central  
 CC nervous and peripheral nervous systems (CNS and PNS). The polypeptides  
 CC and polynucleotides may be used to treat hyperproliferative,  
 CC cardiovascular, autoimmune, nervous system or infectious disorders e.g.  
 CC cancer, heart disease, rheumatoid arthritis, Alzheimer's disease, HIV  
 CC infection and diabetes mellitus. In particular they are useful for  
 CC preventing, treating or ameliorating a medical condition in a mammal such  
 CC as obesity/eating behaviour disorders, narcolepsy, neurological disease,  
 CC addiction to narcotics, nicotine and alcohol, chronic pain, acute pain,  
 CC migraine headaches and anxiety disorders. The polynucleotides encoding  
 CC the neuropeptide receptor can also be used in gene therapy methods for  
 CC treating such diseases  
 XX  
 SQ Sequence 1278 BP; 220 A; 426 C; 347 G; 285 T; 0 U; 0 Other;

Query Match 95.7%; Score 1084.8; DB 4; Length 1278;  
 Best Local Similarity 99.8%; Pred. No. 8.2e-252;  
 Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60  
 Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
 Qy 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180

Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Db	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG	360
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT	960
Db	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCTCAATGTCCTT	960
Qy	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961	AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020

Search completed: October 15, 2004, 16:01:47  
Job time : 485.963 secs

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 15:25:17 ; Search time 88.8123 Seconds  
 (without alignments)  
 7079.645 Million cell updates/sec

Title: US-10-070-532-5  
 Perfect score: 1133  
 Sequence: 1 atggagccctcagccacccc.....tcctgaccatcggtgccccgg 1133

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
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 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1131.4	99.9	1133	2	US-08-846-705-3	Sequence 3, Appli
2	1131.4	99.9	1133	5	PCT-US95-05616-5	Sequence 5, Appli
3	1128.2	99.6	1170	2	US-08-846-705-1	Sequence 1, Appli
4	1114.4	98.4	1116	4	US-08-462-509B-5	Sequence 5, Appli
5	1086.4	95.9	1209	4	US-08-462-509B-1	Sequence 1, Appli
6	1086.4	95.9	1564	2	US-08-846-705-4	Sequence 4, Appli
7	1086.4	95.9	1564	3	US-08-846-704-1	Sequence 1, Appli
8	1086.4	95.9	1564	3	US-08-846-704-3	Sequence 3, Appli
9	1084.8	95.7	1110	4	US-08-462-509B-3	Sequence 3, Appli
10	1081.6	95.5	1209	5	PCT-US95-05616-1	Sequence 1, Appli



11	1076.8	95.0	1110	5	PCT-US95-05616-3	Sequence 3, Appli
12	697.6	61.6	843	3	US-08-513-974B-375	Sequence 375, App
13	670.6	59.2	789	3	US-08-513-974B-55	Sequence 55, Appl
14	670.6	59.2	789	4	US-09-461-436B-55	Sequence 55, Appl
15	520.8	46.0	1633	3	US-09-119-788-1	Sequence 1, Appli
16	249.2	22.0	9785	4	US-09-479-128-1	Sequence 1, Appli
17	163.2	14.4	1293	3	US-09-255-368-7	Sequence 7, Appli
18	156.2	13.8	1410	3	US-09-255-368-1	Sequence 1, Appli
19	128.4	11.3	168575	4	US-09-426-290-1	Sequence 1, Appli
20	119	10.5	1110	3	US-08-513-974B-31	Sequence 31, Appl
21	119	10.5	1110	3	US-08-776-971-26	Sequence 26, Appl
22	119	10.5	1110	4	US-09-461-436B-31	Sequence 31, Appl
23	119	10.5	1331	3	US-08-513-974B-322	Sequence 322, App
24	119	10.5	1331	3	US-08-776-971-103	Sequence 103, App
25	108.8	9.6	669	3	US-08-513-974B-314	Sequence 314, App
26	108.8	9.6	669	3	US-08-776-971-99	Sequence 99, Appl
27	108.8	9.6	1113	3	US-09-172-353-1	Sequence 1, Appli
28	108.8	9.6	1113	4	US-09-799-955-1	Sequence 1, Appli
29	103.2	9.1	1110	4	US-09-170-496D-25	Sequence 25, Appl
30	103.2	9.1	1110	4	US-09-170-496D-177	Sequence 177, App
31	103.2	9.1	1344	4	US-09-016-434-1295	Sequence 1295, Ap
32	103.2	9.1	1356	1	US-07-978-892A-4	Sequence 4, Appli
33	103.2	9.1	1535	4	US-09-016-434-1051	Sequence 1051, Ap
34	103.2	9.1	1969	1	US-07-937-609-28	Sequence 28, Appl
35	103.2	9.1	1969	3	US-08-029-170-28	Sequence 28, Appl
36	100	8.8	2243	1	US-07-937-609-15	Sequence 15, Appl
37	100	8.8	2243	3	US-08-029-170-15	Sequence 15, Appl
38	98.4	8.7	1621	1	US-08-722-001-13	Sequence 13, Appl
39	98.4	8.7	1776	1	US-08-722-001-29	Sequence 29, Appl
40	98.4	8.7	2002	4	US-09-016-434-1172	Sequence 1172, Ap
41	98.4	8.7	2140	1	US-08-334-698-1	Sequence 1, Appli
42	98.4	8.7	2140	1	US-08-228-932-1	Sequence 1, Appli
43	98.4	8.7	2140	1	US-08-468-939-1	Sequence 1, Appli
44	98.4	8.7	2140	2	US-08-406-855A-1	Sequence 1, Appli
45	98.4	8.7	2140	2	US-08-722-190-1	Sequence 1, Appli

#### ALIGNMENTS

##### RESULT 1

US-08-846-705-3

; Sequence 3, Application US/08846705

; Patent No. 5935814

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,705
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-846-705-3

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Query Match          99.9%; Score 1131.4; DB 2; Length 1133;
Best Local Similarity 99.9%; Pred. No. 9.6e-261;
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
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Db    121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
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Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC 420

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Db	361		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
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Db	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Qy	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Qy	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
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Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT	960
Db	901		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT	960
Qy	961		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1080
Db	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1080
Qy	1081		CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCTGACCATCGTGCCCCGG	1133
Db	1081		CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCTGACCATCGTGCCCCGG	1133

RESULT 2

PCT-US95-05616-5

; Sequence 5, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

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; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05616
; FILING DATE: concurrently
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
PCT-US95-05616-5

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Query Match          99.9%; Score 1131.4; DB 5; Length 1133;
Best Local Similarity 99.9%; Pred. No. 9.6e-261;
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGACCCC 60

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy      121 TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
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Db      121 TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
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Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
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Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
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Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
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Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
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Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
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Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
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Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
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Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
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Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
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Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
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Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
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Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080

Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133  
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Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCCTGACCATCGTGCCCCGG 1133

RESULT 3

US-08-846-705-1

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; Sequence 1, Application US/08846705
; Patent No. 5935814
; GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: RATNER & PRESTIA
;     STREET: P.O. BOX 980
;     CITY: VALLEY FORGE
;     STATE: PA
;     COUNTRY: USA
;     ZIP: 19482
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/846,705
;     FILING DATE: 30-APR-1997
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: PRESTIA, PAUL F
;     REGISTRATION NUMBER: 23,031
;     REFERENCE/DOCKET NUMBER: GH-70003
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 610-407-0700
;     TELEFAX: 610-407-0701
;     TELEX: 846169
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1170 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
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US-08-846-705-1

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Query Match          99.6%; Score 1128.2; DB 2; Length 1170;
Best Local Similarity 99.7%; Pred. No. 5.6e-260;
Matches 1130; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db 61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
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 Db 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCC 180  
 Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
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 Db 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
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 Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
 Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
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 Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
 Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
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 Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
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 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
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 Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
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 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 |||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080

Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCTGCTGACCATCGTGCCCCGG 1133  
 |||  
 Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGCTCTGTCTGCTGCCCCATCGTGCCCCGG 1133

#### RESULT 4

US-08-462-509B-5

; Sequence 5, Application US/08462509B

; Patent No. 6410701

#### ; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

#### ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

#### ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

#### ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,509B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

#### ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/05616

; FILING DATE: 05-MAY-1995

#### ; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1

#### ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

#### ; INFORMATION FOR SEQ ID NO: 5:

#### ; SEQUENCE CHARACTERISTICS:

; LENGTH: 1116 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

#### ; FEATURE:

; NAME/KEY: CDS



; LOCATION: 1..1116  
US-08-462-509B-5

Query Match 98.4%; Score 1114.4; DB 4; Length 1116;  
Best Local Similarity 99.9%; Pred. No. 1.1e-256;  
Matches 1115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGACCCC 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCTTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCTTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCCTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCCTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGGGAAGCGC 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTCCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 AAGAGGGTGTTCCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116  
 ||||||||||||||||||||||||||||||||||||  
 Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116

RESULT 5

US-08-462-509B-1

; Sequence 1, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,509B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/05616

; FILING DATE: 05-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

```

; REFERENCE/DOCKET NUMBER: PF168P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1209 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1209
US-08-462-509B-1

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Query Match          95.9%; Score 1086.4; DB 4; Length 1209;
Best Local Similarity 99.9%; Pred. No. 5.2e-250;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy      121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

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Db	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Qy	661		ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	661		ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Db	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC	780
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Qy	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Qy	901		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	901		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Qy	961		AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Db	961		AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020
Qy	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Db	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC	1080
Qy	1081		CTCAGTGG	1088
Db	1081		CTCAGTGG	1088

RESULT 6

US-08-846-705-4

; Sequence 4, Application US/08846705

; Patent No. 5935814

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,705
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1564 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-846-705-4

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Query Match          95.9%; Score 1086.4; DB 2; Length 1564;
Best Local Similarity 99.9%; Pred. No. 5.6e-250;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
        |||
Db      154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        |||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        |||
Db      274 TACCCAAAACAGTATGAGTGGGTCCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        |||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        |||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        |||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

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Db	514		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	480
Db	574		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCGGCGG	633
Qy	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054		ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC	1020
Db	1114		AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTC	1173
Qy	1021		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC	1080
Db	1174		ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAAC TTC	1233
Qy	1081		CTCAGTGG	1088
Db	1234		CTCAGTGG	1241

RESULT 7

US-08-846-704-1

; Sequence 1, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.  
 ; APPLICANT: ELLIS, CATHERINE E.  
 ; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: RATNER & PRESTIA  
 ; STREET: P.O. BOX 980  
 ; CITY: VALLEY FORGE  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19482  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/846,704  
 ; FILING DATE: 30-APR-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PRESTIA, PAUL F  
 ; REGISTRATION NUMBER: 23,031  
 ; REFERENCE/DOCKET NUMBER: GH-70002  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-407-0700  
 ; TELEFAX: 610-407-0701  
 ; TELEX: 846169  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1564 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 US-08-846-704-1

Query Match 95.9%; Score 1086.4; DB 3; Length 1564;  
 Best Local Similarity 99.9%; Pred. No. 5.6e-250;  
 Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
      |||
Db      154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
      |||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC 180
      |||
Db      274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

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Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	960
Db	1054	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCTGCTTC	1020
Db	1114	AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCTGCTTC	1173
Qy	1021	ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTC	1080



Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233  
Qy 1081 CTCAGTGG 1088  
| | | | | | | |  
Db 1234 CTCAGTGG 1241

RESULT 8

US-08-846-704-3.

; Sequence 3, Application US/08846704  
; Patent No. 6020157  
; GENERAL INFORMATION:  
; APPLICANT: BERGSMA, DERK J.  
; APPLICANT: ELLIS, CATHERINE E.  
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/846,704  
; FILING DATE: 30-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-70002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1564 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-846-704-3

Query Match 95.9%; Score 1086.4; DB 3; Length 1564;  
Best Local Similarity 99.9%; Pred. No. 5.6e-250;  
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60

Db	154		ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61		TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214		TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	273
Qy	121		TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	180
Db	274		TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC	333
Qy	181		CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334		CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241		ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394		ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301		CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	360
Db	454		CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG	513
Qy	361		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514		GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574		GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634		GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694		GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754		GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814		ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874		AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934		CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841		CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900

Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1114 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233  
 Qy 1081 CTCAGTGG 1088  
 |||||||  
 Db 1234 CTCAGTGG 1241

RESULT 9

US-08-462-509B-3

; Sequence 3, Application US/08462509B  
 ; Patent No. 6410701  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soppet, Daniel et al  
 ; TITLE OF INVENTION: Human Neuropeptide Receptor  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: MD  
 ; COUNTRY: USA  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/462,509B  
 ; FILING DATE: 05-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/US95/05616  
 ; FILING DATE: 05-MAY-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Wales, Michele M.  
 ; REGISTRATION NUMBER: 43,975  
 ; REFERENCE/DOCKET NUMBER: PF168P1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 301-309-8504  
 ; TELEFAX: 301-309-8439  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1110 base pairs  
 ; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1110
US-08-462-509B-3
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Query Match          95.7%; Score 1084.8; DB 4; Length 1110;
Best Local Similarity 99.8%; Pred. No. 1.2e-249;
Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy      961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080

Qy      1081 CTCAGTGG 1088
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Db      1081 CTCAGTGG 1088

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RESULT 10

PCT-US95-05616-1

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; Sequence 1, Application PC/TUS9505616
; GENERAL INFORMATION:
;   APPLICANT: LI, ET AL.
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;     ADDRESSEE: CECCHI, STEWART & OLSTEIN
;     STREET: 6 BECKER FARM ROAD
;     CITY: ROSELAND
;     STATE: NEW JERSEY
;     COUNTRY: USA
;     ZIP: 07068
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 INCH DISKETTE
;   COMPUTER: IBM PS/2
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/05616
;   FILING DATE: concurrently
;   CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

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Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
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 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||||  
 Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGC 780  
 ||  
 Db 721 AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAGCGC 780  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 |||||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
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 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
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 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 |||||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 Qy 1081 CTCAGTGG 1088  
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 Db 1081 CTCAGTGG 1088

RESULT 11

PCT-US95-05616-3

; Sequence 3, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

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;   OPERATING SYSTEM:  MS-DOS
;   SOFTWARE:  WORD PERFECT 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US95/05616
;   FILING DATE:  concurrently
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  FERRARO, GREGORY D.
;   REGISTRATION NUMBER:  36,134
;   REFERENCE/DOCKET NUMBER:  325800-268
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  201-994-1700
;   TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1110 BASE PAIRS
;   TYPE:  NUCLEIC ACID
;   STRANDEDNESS:  SINGLE
;   TOPOLOGY:  LINEAR
;   MOLECULE TYPE:  cDNA
PCT-US95-05616-3

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Query Match          95.0%;  Score 1076.8;  DB 5;  Length 1110;
Best Local Similarity 99.4%;  Pred. No. 1e-247;
Matches 1081;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db    421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

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Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCT 540  
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 Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 ||||| ||| |||||  
 Db 541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 ||||| |||||  
 Db 601 CTCTGTTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||||  
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
 |||||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGAGAGCCCCAGCCCCGGGGC 840  
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 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACCGGAGGAAGACAGCCAAGATGCTG 900  
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 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACCGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 |||||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080

Qy 1081 CTCAGTGG 1088  
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 Db 1081 CTCAGTGG 1088

RESULT 12

US-08-513-974B-375

; Sequence 375, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji  
 ; APPLICANT: Hosoya, Masaki  
 ; APPLICANT: Fujii, Ryo  
 ; APPLICANT: Ohtaki, Tetsuya  
 ; APPLICANT: Fukusumi, Shoji  
 ; APPLICANT: Ohgi, Kazuhiro

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
; NUMBER OF SEQUENCES: 380  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/513,974B  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP95/01599  
; FILING DATE: 10-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-093989  
; FILING DATE: 19-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-057186  
; FILING DATE: 16-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-007177  
; FILING DATE: 20-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-326611  
; FILING DATE: 28-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-270017  
; FILING DATE: 02-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236357  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236356  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189274  
; FILING DATE: 11-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189273  
; FILING DATE: 11-AUG-1945  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189272  
; FILING DATE: 11-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 45753  
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 843 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..816
US-08-513-974B-375

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Query Match          61.6%; Score 697.6; DB 3; Length 843;
Best Local Similarity 89.9%; Pred. No. 2.4e-157;
Matches 748; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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Qy      312 GCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCTA 371
      ||||| ||||| || | ||||| | | ||||| ||||| ||||| ||
Db      69 GCTGGTAGACATCACGGAATCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTA 128

Qy      372 TCTACAGGCTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCG 431
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      129 TCTACAGGCCGTGTCCGTGTCACTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCG 188

Qy      432 CTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTC 491
      ||||| ||||| ||||| || | ||||| ||||| ||||| ||||| ||
Db      189 CTGGTACGCCATCTGCCACCCGCTGTTGTTCAAGAGCACTGCCCGGCGGCGCCGCGGCTC 248

Qy      492 CATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGA 551
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      249 CATCCTCGGCATCTGGGCGGTGTCGCTGGCTGTCATGGTGCCCTCAGGCTGCTGTCATGGA 308

Qy      552 ATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGA 611
      || ||||| ||||| |||| | ||||| || | || | || ||||| ||
Db      309 GTGTAGCAGCGTGCTGCCCGAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGA 368

Qy      612 ACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTA 671
      ||||| ||||| |||| | ||||| ||||| ||||| ||||| ||
Db      369 GCGCTGGGCAGACGACCTGTACCCCAAGATCTACCACAGCTGCTTCTTCATTGTACCTA 428

Qy      672 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGG 731
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Db      429 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGG 488

Qy      732 CCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAACTGGAAGCGCCCCCTCAGACCA 791
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Db      489 CCGCCAGATCCCCGGCACCACTCGGCCCTGGTGCGCAACTGGAAGCGCCCCCTCAGACCA 548

Qy      792 GCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCT 851
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; FILING DATE: 16-MAR-1995

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-513-974B-55

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Query Match          59.2%; Score 670.6; DB 3; Length 789;
Best Local Similarity 90.6%; Pred. No. 6.5e-151;
Matches 715; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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Qy      271 GCTGACGTTCTGGTGA CTGCTATCTGCCTGCCGCCAGCCTGCTGGTGGACATCACTGAG 330
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Qy      331 TCCTGGCTGTTTCGCCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
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Db      61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy      391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATGCCATCTGCCAC 450
          ||||| |||| | ||||| ||||| ||||| ||||| ||||| ||
Db      121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy      451 CCACTATTGTTCAAGAGCACAGCCCGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510

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; STREET: 101 Federal Street
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02209
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,436B
; FILING DATE: 14-Dec-1999
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/513,974
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; APPLICATION NUMBER: 7-093989
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, DAVID G.
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV2
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
;
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-461-436B-55

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Query Match

59.2%; Score 670.6; DB 4; Length 789;

Best Local Similarity 90.6%; Pred. No. 6.5e-151;

Qy		271	GCTGACGTTCTCTGGTGAAGCTGCTATGCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG	330
Db		1	GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA	60
Qy		331	TCCTGGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCCTATCTACAGGCTGTGTCCGTG	390
Db		61	TCCTGGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCCTATCTACAGGCCGTGTCCGTG	120
Qy		391	TCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATGCCATCTGCCAC	450
Db		121	TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC	180
Qy		451	CCACTATTGTTCAAGAGCACAGCCCGCGGGGCCGTGGCTCCATCCTGGGCATCTGGGCT	510
Db		181	CCGCTGTTGTTCAAGAGCACTGCCC GGCGCGCCGCGGCTCCATCCTCGGCATCTGGGCG	240
Qy		511	GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT	570
Db		241	GTGTCGCTGGCTGT CATGGTGCCCTCAGGCTGCTGT CATGGAGTGTAGCAGCGTGTGCC	300
Qy		571	GAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACC TC	630
Db		301	GAGCTGGCCAACCGCACCCGCCCTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG	360
Qy		631	TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCCCACTGGGCCTC	690
Db		361	TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTACCTACCTGGCCCCACTGGGCCTC	420
Qy		691	ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC	750
Db		421	ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC	480
Qy		751	ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCTCAGACCAGCTGGGGGACCTGGAGCAG	810
Db		481	ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG	540
Qy		811	GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG	870
Db		541	GGCCTGAGCTCAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCCGAGGTGAAACAGATG	600
Qy		871	CGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGC	930
Db		601	CGAGCCCGGAGGAAGACGSCCAAGATGCTGATGGTGGTGTGCTGGTCTTCGCCCTCTGC	660
Qy		931	TACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTTCGGGATGTTCCGCCAAGCC	990
Db		661	TACCTGCCCATCAGTGTCTCAACGTCTCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC	720
Qy		991	AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC	1050
Db		721	AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC	780
Qy		1051	AGCGCTGCC	1059



Db 781 AGCGCCGCC 789

RESULT 15

US-09-119-788-1

; Sequence 1, Application US/09119788

; Patent No. 6166193

; GENERAL INFORMATION:

; APPLICANT: Yanagisawa, Masashi

; TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES

; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: United States of America

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/119,788

; FILING DATE: 21-JUL-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/053,790

; FILING DATE: 25-JUL-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: King, William T

; REGISTRATION NUMBER: 30,954

; REFERENCE/DOCKET NUMBER: GH50029

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5515

; TELEFAX: 610-270-5090

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1633 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA

US-09-119-788-1

Query Match 46.0%; Score 520.8; DB 3; Length 1633;

Best Local Similarity 70.5%; Pred. No. 4.2e-115;

Matches 712; Conservative 0; Mismatches 292; Indels 6; Gaps 1;

Qy 80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139

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Db 217 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGAATACCTGCACCCGAAAGAATATGAGT 276

Qy 140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199

Db	277	GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTGCTGGCTCTCATTGGGAACGTCCTGG	336
Qy	200	TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA	259
Db	337	TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA	396
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTGAAGTCTATCTGCCTGCCGGCCAGCCTGCTGGTGG	319
Db	397	ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCTGG	456
Qy	320	ACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG	379
Db	457	ATATCACTGAGACCTGGTTTTTTTGGACAGTCCCTTTGCAAAGTGATTTCCTTATCTACAGA	516
Qy	380	CTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG	439
Db	517	CCGTGTCGGTGTCTGTGTCTGTCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG	576
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG	499
Db	577	CAATCTGTCAACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA	636
Qy	500	GCATCTGGGCTGTGTGCTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA	559
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Qy	560	GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG	619
Db	697	CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG	756
Qy	620	CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC	679
Db	757	GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC	816
Qy	680	CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCAAGCTCTGGGGCCGCCAGA	739
Db	817	CACTGTGTCTCATGGTGTGGCTTATCTGCAAATATTCGCAAACCTCTGGTGTGACAGA	876
Qy	740	TCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGCCCTCAGACCAGCTGGGGG	799
Db	877	TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC-----TGCAGCCTGTTT	930
Qy	800	ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG	859
Db	931	CACAACCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGGGCGCTGTGGCGGCTGAAA	990
Qy	860	TGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT	919
Db	991	TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT	1050
Qy	920	TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT	979
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Job time : 90.8123 secs

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              (without alignments)
              9829.265 Million cell updates/sec
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	$\frac{9}{8}$ Query
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1	1131.4	99.9	1133	10	US-09-393-696-5	Sequence 5, Appli
2	1114.4	98.4	1116	14	US-10-077-874-5	Sequence 5, Appli
3	1086.4	95.9	1564	15	US-10-225-567A-367	Sequence 367, App
4	1086.4	95.9	1564	16	US-10-352-684A-21	Sequence 21, Appl
5	1084.8	95.7	1110	14	US-10-077-874-3	Sequence 3, Appli
6	1084.8	95.7	1209	14	US-10-077-874-1	Sequence 1, Appli
7	1084.8	95.7	1564	9	US-09-828-538-23	Sequence 23, Appl
8	1081.6	95.5	1209	10	US-09-393-696-1	Sequence 1, Appli
9	1081.6	95.5	1278	11	US-09-826-509-548	Sequence 548, App
10	1076.8	95.0	1110	10	US-09-393-696-3	Sequence 3, Appli
11	912	80.5	1281	9	US-09-730-931-1	Sequence 1, Appli
12	670.6	59.2	789	15	US-10-278-087A-55	Sequence 55, Appl
13	520.8	46.0	1633	15	US-10-282-717-1	Sequence 1, Appli
14	520.8	46.0	1843	15	US-10-225-567A-369	Sequence 369, App
15	516	45.5	1335	11	US-09-826-509-550	Sequence 550, App
16	249.2	22.0	9785	9	US-09-961-848-1	Sequence 1, Appli
17	249.2	22.0	10453	9	US-09-828-538-21	Sequence 21, Appl
18	244	21.5	244	9	US-09-828-538-6	Sequence 6, Appli
19	225.4	19.9	227	9	US-09-828-538-10	Sequence 10, Appl
20	197.4	17.4	356	9	US-09-828-538-2	Sequence 2, Appli
21	179	15.8	179	9	US-09-828-538-4	Sequence 4, Appli
22	163.2	14.4	1290	17	US-10-719-587-55	Sequence 55, Appl
23	163.2	14.4	1290	17	US-10-719-587-56	Sequence 56, Appl
24	163.2	14.4	1293	9	US-09-866-248A-7	Sequence 7, Appli
25	163.2	14.4	1293	15	US-10-225-567A-657	Sequence 657, App
26	163.2	14.4	1320	9	US-09-292-973-3	Sequence 3, Appli
27	156.2	13.8	1299	17	US-10-719-587-38	Sequence 38, Appl
28	156.2	13.8	1410	9	US-09-866-248A-1	Sequence 1, Appli
29	149.8	13.2	1532	9	US-09-292-973-1	Sequence 1, Appli
30	128.4	11.3	168575	15	US-10-178-194-1	Sequence 1, Appli
31	124.4	11.0	977	12	US-09-876-143-1561	Sequence 1561, Ap
32	122	10.8	122	9	US-09-828-538-12	Sequence 12, Appl
33	120.6	10.6	1174	17	US-10-611-210-9	Sequence 9, Appli
34	119.8	10.6	1174	17	US-10-611-210-7	Sequence 7, Appli
35	119	10.5	1110	14	US-10-044-592-17	Sequence 17, Appl
36	119	10.5	1110	15	US-10-278-087A-31	Sequence 31, Appl
37	119	10.5	1113	15	US-10-225-567A-244	Sequence 244, App
38	119	10.5	1152	17	US-10-611-210-10	Sequence 10, Appl
39	119	10.5	1331	14	US-10-044-592-73	Sequence 73, Appl
40	118.4	10.5	1173	17	US-10-611-210-6	Sequence 6, Appli
41	116	10.2	116	9	US-09-828-538-8	Sequence 8, Appli
42	115.8	10.2	1174	17	US-10-611-210-8	Sequence 8, Appli
43	107.2	9.5	669	14	US-10-044-592-70	Sequence 70, Appl
c 44	105.6	9.3	436	13	US-10-027-632-275272	Sequence 275272,
c 45	105.6	9.3	436	16	US-10-027-632-275272	Sequence 275272,

#### ALIGNMENTS

#### RESULT 1

US-09-393-696-5

; Sequence 5, Application US/09393696

; Publication No. US20030022277A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.  
; TITLE OF INVENTION: Human Neuropeptide Receptor  
; FILE REFERENCE: PF168P2  
; CURRENT APPLICATION NUMBER: US/09/393,696  
; CURRENT FILING DATE: 1999-09-10  
; EARLIER APPLICATION NUMBER: PCT/US95/05616  
; EARLIER FILING DATE: 1995-05-05  
; EARLIER APPLICATION NUMBER: US08/462,509  
; EARLIER FILING DATE: 1995-06-05  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1131)  
US-09-393-696-5

Query Match 99.9%; Score 1131.4; DB 10; Length 1133;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGACCCC 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
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Db    121 TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
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Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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;          COUNTRY: USA
;          ZIP: 20850
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/10/077,874
;          FILING DATE: 20-Feb-2002
;          CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/462,509
;          FILING DATE: 05-JUNE-1995
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Wales, Michele M.
;          REGISTRATION NUMBER: 43,975
;          REFERENCE/DOCKET NUMBER: PF168P1D1
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 301-309-8504
;          TELEFAX: 301-309-8439
;    INFORMATION FOR SEQ ID NO: 5:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 1116 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      MOLECULE TYPE: DNA (genomic)
;      FEATURE:
;        NAME/KEY: CDS
;        LOCATION: 1..1116
;      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-077-874-5

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Query Match          98.4%; Score 1114.4; DB 14; Length 1116;
Best Local Similarity 99.9%; Pred. No. 6.2e-311;
Matches 1115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGACCCC 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
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Db    121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
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 Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 |||  
 Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||  
 Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
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 Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
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 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
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 Db 661 ATTGTCACCTACCTGGCCCCACTGGGCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780  
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 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCCACCTCAGCACTGGTGCGGAAGTGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
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 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
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 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
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 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 |||  
 Db 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
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 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080

Qy 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116  
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 Db 1081 CTCAGTGGATGTAAAGAGAAGAGTCTAGTTCTGTCC 1116

RESULT 3

US-10-225-567A-367

; Sequence 367, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 367

; LENGTH: 1564

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-367

Query Match 95.9%; Score 1086.4; DB 15; Length 1564;

Best Local Similarity 99.9%; Pred. No. 8e-303;

Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db     154 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy     121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
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Db     274 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 333

Qy     181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy     241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db     394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy     301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 513

Qy     361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db     514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

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Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
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 Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633  
 Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 693  
 Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
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 Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
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 Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813  
 Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
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 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
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 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
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 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 1114 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
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 Qy 1081 CTCAGTGG 1088  
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 Db 1234 CTCAGTGG 1241

RESULT 4

US-10-352-684A-21

; Sequence 21, Application US/10352684A

; Publication No. US20030215452A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals Inc.

; APPLICANT: Carroll, Joseph M.

; APPLICANT: Healy, Aileen

```

; APPLICANT: Weich, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303,
13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847,
1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPI02-019P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1431)
US-10-352-684A-21

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Query Match          95.9%; Score 1086.4; DB 16; Length 1564;
Best Local Similarity 99.9%; Pred. No. 8e-303;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 213

Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAACAGTATGAGTGGGTCCTCATCGAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

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Db	274	 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTCTGTCGTGGCC	333
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Db	334	 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCTGGCCATGCCCTCTGCAAG	360
Db	454	 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCTGGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660
Db	754	 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	813
Qy	661	ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	720
Db	814	 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC	873
Qy	721	AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	780
Db	874	 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGAAGCGC	933
Qy	781	CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	840
Db	934	 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC	993
Qy	841	CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	900
Db	994	 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG	1053
Qy	901	ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGTCCTT	960
Db	1054	 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGTCTCAATGTCCTT	1113
Qy	961	AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC	1020

Db 1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
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Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233

Qy 1081 CTCAGTGG 1088  
 |||

Db 1234 CTCAGTGG 1241

RESULT 5

US-10-077-874-3

; Sequence 3, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1110 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1110

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-077-874-3

Query Match 95.7%; Score 1084.8; DB 14; Length 1110;  
Best Local Similarity 99.8%; Pred. No. 2.1e-302;  
Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
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Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540
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Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCAGATATTCCGC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
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 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 |||||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
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 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Qy 1081 CTCAGTGG 1088  
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 Db 1081 CTCAGTGG 1088

RESULT 6

US-10-077-874-1

; Sequence 1, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:





Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
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 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGGAAAGCGC 780  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
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 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
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 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTT 1080  
 Qy 1081 CTCAGTGG 1088  
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 Db 1081 CTCAGTGG 1088

RESULT 7

US-09-828-538-23

; Sequence 23, Application US/09828538

; Patent No. US20010025031A1

; GENERAL INFORMATION:

; APPLICANT: Ellis, Catherine E.

; APPLICANT: Kwok, Cheni

; APPLICANT: Bodsworth, Nicola J.

; APPLICANT: Halsey, Wendy

; APPLICANT: Van Horn, Stephanie

; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods

; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications

; FILE REFERENCE: GH-50038-C1

; CURRENT APPLICATION NUMBER: US/09/828,538

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/088,624

; PRIOR FILING DATE: 1998-06-08

; PRIOR APPLICATION NUMBER: 60/093,726

; PRIOR FILING DATE: 1998-07-22  
 ; PRIOR APPLICATION NUMBER: 09/328,014  
 ; PRIOR FILING DATE: 1999-06-08  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 23  
 ; LENGTH: 1564  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 US-09-828-538-23

Query Match 95.7%; Score 1084.8; DB 9; Length 1564;  
 Best Local Similarity 99.8%; Pred. No. 2.3e-302;  
 Matches 1086; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC	60
Db	154	ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG	213
Qy	61	TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG	120
Db	214	TCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGGATTATCTG	273
Qy	121	TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	180
Db	274	TACCCAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC	333
Qy	181	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	240
Db	334	CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC	393
Qy	241	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	300
Db	394	ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG	453
Qy	301	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGCCATGCCCTCTGCAAG	360
Db	454	CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCCGCCATGCCCTCTGCAAG	513
Qy	361	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	420
Db	514	GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC	573
Qy	421	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	480
Db	574	GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG	633
Qy	481	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	540
Db	634	GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT	693
Qy	541	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	600
Db	694	GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA	753
Qy	601	GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT	660

Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813  
 Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 814 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873  
 Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
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 Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
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 Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1114 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173  
 Qy 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1233  
 Qy 1081 CTCAGTGG 1088  
 ||||||||  
 Db 1234 CTCAGTGG 1241

RESULT 8

US-09-393-696-1

; Sequence 1, Application US/09393696

; Publication No. US20030022277A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; FILE REFERENCE: PF168P2

; CURRENT APPLICATION NUMBER: US/09/393,696

; CURRENT FILING DATE: 1999-09-10

; EARLIER APPLICATION NUMBER: PCT/US95/05616

; EARLIER FILING DATE: 1995-05-05

; EARLIER APPLICATION NUMBER: US08/462,509

; EARLIER FILING DATE: 1995-06-05

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1209

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1209)  
US-09-393-696-1

Query Match 95.5%; Score 1081.6; DB 10; Length 1209;  
Best Local Similarity 99.6%; Pred. No. 1.8e-301;  
Matches 1084; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy    121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TACCCAAAACAGTATGAGTGGGTCTCATCCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy    541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCAGTCATGGAATGCGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db    601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy    661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy    721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACTCAGCACTGGTGCGGAAGTGAAGCGC 780
        || |||||||||||||||||||||||||||||||||||||||||||||||
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Db 721 AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGC GGAACTGGAAGCGC 780  
 Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
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 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
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 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960  
 Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020  
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 Db 1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080  
 Qy 1081 CTCAGTGG 1088  
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 Db 1081 CTCAGTGG 1088

RESULT 9

US-09-826-509-548

; Sequence 548, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 548

; LENGTH: 1278

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-826-509-548

Query Match 95.5%; Score 1081.6; DB 11; Length 1278;  
 Best Local Similarity 99.6%; Pred. No. 1.8e-301;  
 Matches 1084; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60  
 |||  
 Db 1 ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120  
 |||  
 Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180  
 |||  
 Db 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCC 180

Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 |||  
 Db 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
 |||  
 Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360  
 |||  
 Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420  
 |||  
 Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||  
 Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy 481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGTGGCCATCATGGTGCCCCAGGCT 540  
 |||  
 Db 481 GCGCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCGTGGCCATCATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 |||  
 Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||  
 Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||  
 Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780  
 |||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 |||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGACGGAGGAAGACAGCCAAGATGCTG 900

```

      |||
Db      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAAAAAGATGCTG 900
Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
      |||
Db      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
Qy      961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
      |||
Db      961 AAGAGGGTGTTCTGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
      |||
Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
Qy      1081 CTCAGTGG 1088
      |||
Db      1081 CTCAGTGG 1088

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RESULT 10

US-09-393-696-3

; Sequence 3, Application US/09393696

; Publication No. US20030022277A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; FILE REFERENCE: PF168P2

; CURRENT APPLICATION NUMBER: US/09/393,696

; CURRENT FILING DATE: 1999-09-10

; EARLIER APPLICATION NUMBER: PCT/US95/05616

; EARLIER FILING DATE: 1995-05-05

; EARLIER APPLICATION NUMBER: US08/462,509

; EARLIER FILING DATE: 1995-06-05

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 1110

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1110)

US-09-393-696-3

Query Match 95.0%; Score 1076.8; DB 10; Length 1110;

Best Local Similarity 99.4%; Pred. No. 4.3e-300;

Matches 1081; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCC 60
      |||
Db      1 ATGGAGCCCTCAGCCACCCAGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGCCG 60
Qy      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
      |||
Db      61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

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Qy 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180  
 |||  
 Db 121 TACCCAAAACAGTATGAGTGGGTCTCATCGCAGCCTATGTGGCTGTGTTTCGTCTGGCC 180

Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240  
 |||  
 Db 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300  
 |||  
 Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360  
 |||  
 Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCA GTGGCAGTGCTAACTCTCAGCTTCATC 420  
 |||  
 Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCA GTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480  
 |||  
 Db 421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540  
 |||  
 Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCT 540

Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600  
 |||  
 Db 541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660  
 |||  
 Db 601 CTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720  
 |||  
 Db 661 ATTGTACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACCTGGAAGCGC 780  
 |||  
 Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACCTGGAAGCGC 780

Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840  
 |||  
 Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900  
 |||  
 Db 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960  
 |||  
 Db 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCATCAGCGTCCTCAATGTCCTT 960

Qy 961 AAGAGGGTGTTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

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Db          961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
Qy          1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
Db          1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTC 1080
Qy          1081 CTCAGTGG 1088
Db          1081 CTCAGTGG 1088

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RESULT 11

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US-09-730-931-1
; Sequence 1, Application US/09730931
; Patent No. US20020064814A1
; GENERAL INFORMATION:
; APPLICANT: ELLIS, CATHERINE E.
; TITLE OF INVENTION: DOG OREXIN 1 RECEPTOR
; FILE REFERENCE: GH-70669
; CURRENT APPLICATION NUMBER: US/09/730,931
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/169,373
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: CANIS FAMILIARIS
US-09-730-931-1

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Query Match          80.5%; Score 912; DB 9; Length 1281;
Best Local Similarity 90.3%; Pred. No. 1.5e-252;
Matches 988; Conservative 0; Mismatches 100; Indels 6; Gaps 1;

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Qy          1 ATGGAGCCCTCAGCCACCCAGGGGGCCAGATGGGGGTCCCCCTGGCAGCAGAGAGAGCCC 60
Db          1 ATGGAGCCCTCAGCCACCCAGGGGGCCAGACTGGGACCCCAACGGCGGGCGGGGAGCTG 60

Qy          61 TCCCCT-----GTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGAT 114
Db          61 TCTCCGTCACTGGTGCCTCCCGACTATGAAGACGAGTTCCTGCGCTATCTGTGGCGCGAT 120

Qy          115 TATCTGTACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTC 174
Db          121 TACCTGTACCCAAAGCAGTATGAGTGGGTCCTCATCGCTGCCTACGTGGCTGTGTTTCCTA 180

Qy          175 GTGGCCCTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGG 234
Db          181 GTGGCCCTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGAGGAACCACCACATGAGG 240

Qy          235 ACAGTCACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATC 294
Db          241 ACGGTCACCAACTATTTTCATTGTCAACCTGTCCCTGGCTGATGTGCTGGTGACAGCCATC 300

Qy          295 TGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTC 354

```



US-10-278-087A-55  
; Sequence 55, Application US/10278087A  
; Publication No. US20030138817A1  
; GENERAL INFORMATION:  
; APPLICANT: Shuji Hinuma  
; Yasuaki Ito  
; Ryo Fujii  
; TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
; Production, And Use Thereof  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Edwards & Angell, LLP  
; STREET: 101 Federal Street  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02209  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/278,087A  
; FILING DATE: 31-Jan-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/461,436  
; FILING DATE: 14-DEC-1999  
; APPLICATION NUMBER: 09/038,572  
; FILING DATE: 11-MAR-1998  
; APPLICATION NUMBER: 08/513,974  
; FILING DATE: 14-SEP-1995  
; APPLICATION NUMBER: PCT/JP95/01599  
; FILING DATE: 10-AUG-1995  
; APPLICATION NUMBER: 7-093989  
; FILING DATE: 19-APR-1995  
; APPLICATION NUMBER: 7-057186  
; FILING DATE: 16-MAR-1995  
; APPLICATION NUMBER: 7-007177  
; FILING DATE: 20-JAN-1995  
; APPLICATION NUMBER: 6-326611  
; FILING DATE: 28-DEC-1994  
; APPLICATION NUMBER: 6-270017  
; FILING DATE: 02-NOV-1994  
; APPLICATION NUMBER: 6-236357  
; FILING DATE: 30-SEP-1994  
; APPLICATION NUMBER: 6-236356  
; FILING DATE: 30-SEP-1994  
; APPLICATION NUMBER: 6-189274  
; FILING DATE: 11-AUG-1994  
; APPLICATION NUMBER: 6-189273  
; FILING DATE: 11-AUG-1994  
; APPLICATION NUMBER: 6-189272  
; FILING DATE: 11-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CONLIN, DAVID G.

```

;      REGISTRATION NUMBER: <Unknown>
;      REFERENCE/DOCKET NUMBER: 45753 DIV3
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 617-439-4444
;      TELEFAX: 617-439-4170
;      INFORMATION FOR SEQ ID NO: 55:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 789 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;      MOLECULE TYPE: cDNA
;      SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-278-087A-55

```

Qy 80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139  
| | | | | | | | | | | | | | | | | | | | | | |  
Db 217 ACGACGAGGAATTCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 276

Qy 140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199  
| | | | | | | | | | | | | | | | | | | | | | |  
Db 277 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 336

Qy 200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259

Db	337	TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA	396
Qy	260	ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG	319
Db	397	ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG	456
Qy	320	ACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCATCTACAGG	379
Db	457	ATATCACTGAGACCTGGTTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCCTTATCTACAGA	516
Qy	380	CTGTGTCCGTGTCACTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG	439
Db	517	CCGTGTGGTGTCTGTGTCTGTCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG	576
Qy	440	CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGCGGGCCCGTGGCTCCATCCTGG	499
Db	577	CAATCTGTACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTTGTCA	636
Qy	500	GCATCTGGGCTGTGTGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA	559
Db	637	TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA	696
Qy	560	GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG	619
Db	697	CCGTGTTCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG	756
Qy	620	CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC	679
Db	757	GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC	816
Qy	680	CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCAAGCTCTGGGGCCGCCAGA	739
Db	817	CACTGTGTCTCATGGTGTGGCTTATCTGCAAATATTTGCAAACCTCTGGTGTGACAGA	876
Qy	740	TCCCCGGCACCACCTCAGCACTGGTGCGGAAGTGGAAAGCGCCCCCTCAGACCAGCTGGGGG	799
Db	877	TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC-----TGCAGCCTGTTT	930
Qy	800	ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG	859
Db	931	CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGGGCGCTGTGGCGGCTGAAA	990
Qy	860	TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT	919
Db	931	TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTGTCTTTTGGTAT	1050
Qy	920	TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTTCGGGATGT	979
Db	1051	TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT	1110
Qy	980	TCCGCCAAGCCAGTGACCGGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG	1039
Db	1111	TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG	1170
Qy	1040	TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTTCCTCAGTGA	1089

Db 1171 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGGA 1220

RESULT 14

US-10-225-567A-369

; Sequence 369, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 369

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-369

Query Match 46.0%; Score 520.8; DB 15; Length 1843;

Best Local Similarity 70.5%; Pred. No. 1e-139;

Matches 712; Conservative 0; Mismatches 292; Indels 6; Gaps 1;

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Qy      80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAACAGTATGAGT 139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     428 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 487

Qy     140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     488 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 547

Qy     200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     548 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 607

Qy     260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     608 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCAGCCACACTGGTCGTGG 667

Qy     320 ACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCTATCTACAGG 379
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     668 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCTTATCTACAGA 727

Qy     380 CTGTGTCCGTGTGAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     728 CCGTGTGCGGTGTCTGTGTCTGTCTCCTCACACTGAGCTGTATCGCCTGGATCGGTGGTATG 787

Qy     440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGGGGCCCGTGGCTCCATCCTGG 499
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db 788 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 847  
 Qy 500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559  
 ||||| ||| || || ||| || ||||| |||||  
 Db 848 TCATCTGGATTGTCTCCTGCATTATAATGATTCCCTCAGGCCATCGTCATGGAGTGCAGCA 907  
 Qy 560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619  
 ||| ||| || ||||| || ||||| || ||||| |||||  
 Db 908 CCGTGTTCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 967  
 Qy 620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC 679  
 | ||| | ||||| ||||| || ||||| || || ||| ||| |  
 Db 968 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 1027  
 Qy 680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATCCGCAAGCTCTGGGGCCGCCAGA 739  
 |||| | ||||| ||| ||| || ||||| ||||| || ||| |||  
 Db 1028 CACTGTGTCTCATGGTGTGGCTTATCTGCAAATATTCGCAAACCTCTGGTGTGCACAGA 1087  
 Qy 740 TCCCCGGCACCACTCAGCACTGGTGCGGAACCTGGAAGCGCCCTCAGACCAGCTGGGGG 799  
 |||| || || | || | || | || || ||||| || |||||  
 Db 1088 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC-----TGCAGCCTGTTT 1141  
 Qy 800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCTGGCTGAAG 859  
 | | | ||| | | | || ||||| |||| | |||||  
 Db 1142 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA 1201  
 Qy 860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919  
 | ||||| || || | |||| ||||| |||| ||||| |||| |  
 Db 1202 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 1261  
 Qy 920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979  
 | || ||||| || || || || ||||| || ||||| || |||||  
 Db 1262 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1321  
 Qy 980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039  
 | ||| | ||| || || |||| || ||||| || ||||| || |||||  
 Db 1322 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1381  
 Qy 1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACCTCCTCAGTGGA 1089  
 | || |||| || |||| || || || || || || || |||||  
 Db 1382 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGGA 1431

RESULT 15

US-09-826-509-550

; Sequence 550, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

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; PRIOR APPLICATION NUMBER: 60/195,747  
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; NUMBER OF SEQ ID NOS: 589  
; SOFTWARE: PatentIn Version 2.1  
; SEQ ID NO 550  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-826-509-550

Query Match 45.5%; Score 516; DB 11; Length 1335;  
Best Local Similarity 70.2%; Pred. No. 2.3e-138;  
Matches 709; Conservative 0; Mismatches 295; Indels 6; Gaps 1;

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Qy      80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Db     104 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 163

Qy     140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTTCGTTCGTGGCCCTGGTGGGCAACACGCTGG 199
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Db     164 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTTCGTGGCTCTCATTGGGAACGTCCTGG 223

Qy     200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
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Db     224 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 283

Qy     260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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Db     284 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 343

Qy     320 ACATCACTGAGTCCTGGCTGTTTCGGCCATGCCCTCTGCAAGGTCATCCCCATCTACAGG 379
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Db     344 ATATCACTGAGACCTGGTTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCCTTATCTACAGA 403

Qy     380 CTGTGTCCGTGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     404 CCGTGTGCGGTGTCTGTGTCTGTTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 463

Qy     440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Db     464 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 523

Qy     500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
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Db     524 TCATCTGGATTGTCTCCTGCATTATAATGATTCCCTCAGGCCATCGTCATGGAGTGCAGCA 583

Qy     560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
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Db     584 CCGTGTTCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 643

Qy     620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTACCTACCTGGCCC 679
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Db     644 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGCTGACATACATGGCAC 703

Qy     680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCGCAAGCTCTGGGGCCGCCAGA 739
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